

49753

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: KAREN A. CANELLA Examiner #: 77681 Date: 8/28/01
 Art Unit: 1642 Phone Number 308-5362 Serial Number: 691503, 089
 Mail Box and Bldg/Room Location: 8D 03 Results Format Preferred (circle) PAPER DISK E-MAIL
8E12

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers; and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

SEARCH AND INTERFERENCE SEARCH

IN THE PROTEIN DATABASES ONLY

- ① SEQ ID NO: 2
- ② SEQ ID NO: 4
- ③ SEQ ID NO: 5

suffix Aug 28

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Type of Search

Vendors and cost where applicable

Searcher: Ch. Hines NA Sequence (#) _____ STN _____
 Searcher Phone #: 308-5501 TAA Sequence (#) 3 Dialog _____
 Searcher Location: Biology Lab Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: 8/28/01 Bibliographic _____ Dr. Link _____
 Date Completed: 8/31/01 Litigation _____ Lexis/Nexis _____
 Searcher Prep & Review Time: _____ Fulltext _____ Sequence Systems ABSS62
 Clerical Prep Time: 5 min Patent Family _____ WWW/Internet _____
 Online Time: 3 min Other _____ Other (specify) _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:11:14 ; Search time 242.67 Seconds

(without alignments)
360.192 Million cell updates/sec

Title: US-09-503-089A-5

Perfect score: 2042
Sequence: 1 MKRONVRLALIVCTFTYLL.....STGLHSLSTFNGIMKRSSV 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Pending_Patents_AA_Main:*
- 1: /cgn2_6/ptodata/2/paa/PCTUS.COMB.pep:*
- 2: /cgn2_6/ptodata/2/paa/US06.COMB.pep:*
- 3: /cgn2_6/ptodata/2/paa/US07.COMB.pep:*
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- 6: /cgn2_6/ptodata/2/paa/US082.COMB.pep:*
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- 22: /cgn2_6/ptodata/2/paa/US098.COMB.pep:*
- 23: /cgn2_6/ptodata/2/paa/US099.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2042	100.0	394	15	US-09-144-914-4
2	2042	100.0	394	18	US-09-436-265-4
3	2042	100.0	394	19	US-09-503-089A-5
4	2042	100.0	394	20	US-09-655-272-5
5	1819	89.1	405	15	US-09-144-914-5
6	1819	89.1	405	18	US-09-436-265-5
7	1235.5	60.5	309	12	US-08-816-011C-55
8	1235.5	60.5	309	12	US-08-816-011C-62
9	1224	59.9	312	12	US-08-816-011-55
10	1224	59.9	312	12	US-08-816-011A-55

11	1116	54.7	374	19	US-09-516-279-4	Sequence 2, Appl1
12	1116	54.7	374	19	US-09-516-279-4	Sequence 4, Appl1
13	1116	54.7	374	23	US-60-199-020-2	Sequence 2, Appl1
14	846	41.4	400	19	US-09-518-866-7	Sequence 5, Appl1
15	838	41.0	400	19	US-09-518-866-7	Sequence 2, Appl1
16	838	41.0	400	23	US-60-203-495-1	Sequence 1, Appl1
17	777	38.1	339	23	US-60-161-932-1	Sequence 1980, Ap
18	777	38.1	340	23	US-60-167-245-7	Sequence 700, Ap
19	777	38.1	340	23	US-60-173-464-1	Sequence 16346, A
20	777	38.1	340	23	US-60-191-637-1	Sequence 19979, A
21	777	37.9	340	23	US-60-191-681-1	Sequence 15731, A
22	774	37.9	279	1	PCT-US01-00663	Sequence 27364, A
23	774	37.9	279	23	US-60-236-359-7	Sequence 15807, A
24	773	37.9	408	1	PCT-US00-20435	Sequence 12, Appl
25	773	37.9	408	17	US-09-362-842-2	Sequence 41787, A
26	742	36.3	398	23	US-60-191-637-7	Sequence 778, Ap
27	619.5	30.3	156	23	US-60-195-134	Sequence 776, Ap
28	615.5	30.1	126	23	US-60-195-134	Sequence 777, Ap
29	591.5	29.0	149	23	US-60-195-134	Sequence 479, Ap
30	475	23.3	170	23	US-60-142-843-7	Sequence 2599, Ap
31	455.5	22.3	101	23	US-60-196-712-7	Sequence 2595, Ap
32	453.5	22.2	101	23	US-60-196-712-7	Sequence 214, Ap
33	441.5	21.6	161	23	US-60-139-670-2	Sequence 529, Ap
34	441.5	21.6	161	23	US-60-140-804	Sequence 529, Ap
35	437	21.4	205	23	US-60-143-874	Sequence 934, Ap
36	432	21.2	114	23	US-60-182-568-8	Sequence 857, Ap
37	427	20.9	110	23	US-60-170-429-3	Sequence 857, Ap
38	414.5	20.3	101	23	US-60-196-712-7	Sequence 2597, Ap
39	382	18.7	102	23	US-60-196-712-7	Sequence 2598, Ap
40	381	18.7	102	23	US-60-196-712-7	Sequence 14, Appl
41	379	18.6	361	1	PCT-US00-20439-1	Sequence 14, Appl
42	379	18.6	361	17	US-09-362-842-2	Sequence 714, Appl
43	372	18.2	98	23	US-60-182-076-7	Sequence 8, Appl1
44	370	18.1	370	15	US-09-144-914-4	Sequence 8, Appl1
45	370	18.1	370	18	US-09-436-265-4	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-144-914-4
: Sequence 4, Application US/09144914
: GENERAL INFORMATION:
: APPLICANT: Duprat, Fabrice
: APPLICANT: Lesage, Fabrice
: APPLICANT: Fink, Michel
: APPLICANT: Lazdunski, Michel
: TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
: FILE REFERENCE: 989.6705CIP
: CURRENT APPLICATION NUMBER: US/09/144,914
: EARLIER APPLICATION NUMBER: 08/7749,816
: EARLIER FILING DATE: 1996-11-15
: EARLIER APPLICATION NUMBER: 60/095,234
: EARLIER FILING DATE: 1998-08-04
: EARLIER APPLICATION NUMBER: FR 96/01565
: EARLIER FILING DATE: 1996-02-08
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 394
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: TASK
US-09-144-914-4
Query Match 100.0%; Score 2042; Length 394;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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RESULT 2
US-09-436-265-4
: Sequence 4, Application US/09436265
: GENERAL INFORMATION:
: APPLICANT: REYES, ROBERTO
: APPLICANT: DUPRAT, FABRICE
: APPLICANT: LESAGE, FLORIAN
: APPLICANT: FINK, MICHEL
: APPLICANT: SALINAS, MIGUEL
: APPLICANT: FARMAN, NICOLETTE
: APPLICANT: LAZDINSKI, MICHEL
: TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR
: TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF
: TITLE OF INVENTION: DRUGS
: FILE REFERENCE: 1201-CIP2-00
: CURRENT APPLICATION NUMBER: US/09/436,265
: CURRENT FILING DATE: 1999-11-08
: PRIOR APPLICATION NUMBER: 60/095,234
: PRIOR FILING DATE: 1998-08-04
: PRIOR APPLICATION NUMBER: 60/107,692
: PRIOR FILING DATE: 1996-11-09
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 394
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: TASK
US-09-436-265-4

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Query Match	100.0%;	Score 2042;	DB 18;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 1.9e-197;		
Matches 394;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

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Db	121	TLVWFOSIGEBINTLVRLILHRAKKGJGMRAVDVSMANV	TFPFCISTLTCIGAAAFSH	180
QY	181	YEHWFEOAYVYCEITLTITIGFGDYVALOKDLOTOPOV	TFVYILTGLTVIGAFLN	240
Db	181	YEHWFEOAYVYCEITLTITIGFGDYVALOKDLOTOPOV	TFVAFSEVYILTGLTVIGAFLN	240
QY	241	LVVLREPMNMNDEDKRPAEHALLTRNGOGGGGGGSAH	DTASTAAGGGGFPNNY	300
Db	241	LVVLREPMNMNDEDKRPAEHALLTRNGOAGGGGGGSAI	DTASTAAGGGGFPNNY	300
QY	301	AEVLHFQSMCGLWYKSKREKLOYISIPMIPDLSTPOTCY	SHSPGGGGRRYSDTPSRR	360
Db	301	AEVLHFQSMCGLWYKSKREKLOYISIPMIPDLSTPOTC	SHSPGGGGRRYSDTPSRR	360
QY	361	CLCSCAPRSALISVSTGLHSLSTRGILMKRRSSV		394
Db	361	CLCSCAPRSALISVSTGLHSLSTRGILMKRRSSV		394

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RESULT 3
US-09-503-089A-5
: Sequence 5, Application US/09503089A
: GENERAL INFORMATION:
: APPLICANT: PATEL, AMANDA J.
: APPLICANT: HONORE, ERIC
: APPLICANT: LESAGE, FLORIAN
: APPLICANT: ROMERY, GEORGES
: APPLICANT: IAZDUSKI, MICHEL
: TITLE OF INVENTION: A method for the identification of anesthetics
: FILE REFERENCE: fl7b1p3prov3-humanantrek
: CURRENT APPLICATION NUMBER: US/09/503,089A
: CURRENT FILING DATE: 2000-02-11
: NUMBER OF SEQ. ID NOS: 5
: SOFTWARE: Microsoft Word 2000
: SEQ ID NO 5
: LENGTH: 394
: TYPE: PRT
: ORGANISM: Mus sp.
: FEATURE:
: OTHER INFORMATION: TASK
US-09-503-089A-5

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Query Match	100.0%;	Score 2042;	F ₁ 19;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 1.9e+137;		
Matches 394;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	KKROVRFVLTALVCTFFYLLVGA	VPALESEPTLEK	TLROELRARNYLSOGGE	60
Db	1	MKRONVRLTALVCTFFYLLVGA	VPALESEPTLEK	TLROELRARNYLSOGGE	60
QY	61	ELERVLTALRKPKAGVOMREAGSF	YFAIVYITTYGAG	TDGKRVCFMYPALLGIDP	120
Db	61	ELERVLTALRKPKAGVOMREAGSF	YFAIVYITTYGAG	TDGKRVCFMYPALLGIDP	120
QY	121	TLVPMOSIGEEINFLVRLRLHRAK	KGGMRAVDVSMNN	IGFSPCISITLIGAAAFSH	180
Db	121	TLVPMOSIGEEINFLVRLRLHRAK	KGGMRAVDVSMNN	IGFSPCISITLIGAAAFSH	180
QY	181	YEHHTFPOAYITTCITLTTIGFGD	YVALOKDOLOTOPQ	YVSFVYILTGLTVIGAFLN	240
Db	181	YEHHTFPOAYITTCITLTTIGFGD	YVALOKDOLOTOPQ	YVSFVYILTGLTVIGAFLN	240
QY	241	LVLTREPMNMNDEKRDAAEHRA	LTLTRNGOAGGGGGSAL	FTPTASTAAAGGCFRRNY	300
Db	241	LVLTREPMNMNDEKRDAAEHRA	LTLTRNGOAGGGGGSAL	FTPTASTAAAGGCFRRNY	300
QY	301	AEVLHFSOMSCMLYKSKREKLOYS	IPMIPRDLSTSTQC	SHSSPFGGGRYSDTPSR	360
Db	301	AEVLHFSOMSCMLYKSKREKLOYS	IPMIPRDLSTSTQC	SHSSPFGGGRYSDTPSR	360

QY 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394
 Db 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 4

US-09-655-272-5
 : Sequence 5, Application US/09655272
 : GENERAL INFORMATION:
 : APPLICANT: HONORE, ERIC
 : APPLICANT: PINK, MICHEL
 : APPLICANT: LAZDUNSKI, MICHEL
 : APPLICANT: LESAGE, FLORIAN
 : APPLICANT: DUPRAT, FABRICE
 : TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
 : TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
 : FILE REFERENCE: 1383-00
 : CURRENT APPLICATION NUMBER: US/09/655, 272
 : CURRENT FILING DATE: 2000-09-05
 : PRIOR APPLICATION NUMBER: PCT/FR99/00404
 : PRIOR FILING DATE: 1999-02-23
 : PRIOR APPLICATION NUMBER: FR 98/02725
 : PRIOR FILING DATE: 1998-03-05
 : NUMBER OF SEQ ID NOS: 5
 : SOFTWARE: Patentln Ver. 2.1
 : SEQ ID NO 5
 : LENGTH: 394
 : TYPE: PRT
 : ORGANISM: Unknown Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of unknown sequence: TASK
 US-09-655-272-5

IFN

Query Match 100.0%; Score 2042; DB 20; Length 394;
 Best Local Similarity 100.0%; Pred. No. 1.9e-197;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVTLIVCTFTYLLVGAAVFDALSEPILRORLEKQOELRARNYLSGGYE 60
 Db 1 MKRONVTLIVCTFTYLLVGAAVFDALSEPILRORLEKQOELRARNYLSGGYE 60
 QY 61 ELERVVLLKPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGCVFPMFYALLGPI 120
 Db 61 ELERVVLLKPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGCVFPMFYALLGPI 120
 QY 121 TLVWFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSH 180
 Db 121 TLVWFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSH 180
 QY 181 YEHTFFQAYVYCFITLTIGFDYVALQDQALQTOPQYVAFSFFVILTLGLTVIGAFLN 240
 Db 181 YEHTFFQAYVYCFITLTIGFDYVALQDQALQTOPQYVAFSFFVILTLGLTVIGAFLN 240
 QY 241 LVVLRFTMAAEDKRAEHRALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNV 300
 Db 241 LVVLRFTMAAEDKRAEHRALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNV 300
 QY 301 AEVLHFOSMCSCLMYKSREKLOYSIPIIPRDLSTSDTCVEOSHSPGGGRTSDPSSR 360
 Db 301 AEVLHFOSMCSCLMYKSREKLOYSIPIIPRDLSTSDTCVEOSHSPGGGRTSDPSSR 360
 QY 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394
 Db 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 5

US-09-144-914-5
 : Sequence 5, Application US/09144914
 : GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice
 APPLICANT: Lesage, Florian
 APPLICANT: Fink, Michel
 APPLICANT: Lazdunski, Michel
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
 TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
 FILE REFERENCE: 989.6705CIP
 CURRENT APPLICATION NUMBER: US/09/144, 914
 CURRENT FILING DATE: 1998-09-01
 EARLIER APPLICATION NUMBER: 08/749, 816
 EARLIER FILING DATE: 1996-11-15
 EARLIER APPLICATION NUMBER: 60/095, 234
 EARLIER FILING DATE: 1998-08-04
 EARLIER APPLICATION NUMBER: FR 96/01565
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 5
 LENGTH: 405
 TYPE: PRT
 ORGANISM: Murine
 FEATURE:
 OTHER INFORMATION: TASK
 US-09-144-914-5

Query Match 89.1%; Score 1819; DB 17; Length 405;
 Best Local Similarity 88.1%; Pred. No. 7.6e-175;
 Matches 357; Conservative 9; Mismatches 2; Indels 14; Gaps 2;

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 Db 1 ENVTALLIVCTFTYLLVGAAVFDALSEPILRORLEKQOELRARNYLSGGYE 60
 QY 64 RYVRLKPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGCVFPMFYALLGPI 123
 Db 61 RYVRLKPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGCVFPMFYALLGPI 120
 QY 124 MFOSLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSHYEH 183
 Db 121 MFOSLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSHYEH 180
 QY 184 WTEFQAYVYCFITLTIGFDYVALQDQALQTOPQYVAFSFFVILTLGLTVIGAFLN 243
 Db 181 WTEFQAYVYCFITLTIGFDYVALQDQALQTOPQYVAFSFFVILTLGLTVIGAFLN 240
 QY 244 LRFPTMAAEDKRAEHRALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNV 291
 Db 241 LRFPTMAAEDKRAEHRALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNV 300
 QY 292 -GGGGRFNNVYAEVLHFOSMCSCLMYKSREKLOYSIPIIPRDLSTSDTCVEOSHSPGG 349
 Db 301 GVGSGFRNNVYAEVLHFOSMCSCLMYKSREKLOYSIPIIPRDLSTSDTCVEOSHSPGG 360
 QY 350 GGRYDTPSRCLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394
 Db 361 GGRYDTPSRCLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 6

US-09-436-265-5
 : Sequence 5, Application US/09436265
 : GENERAL INFORMATION:
 : APPLICANT: REYES, ROBERTO
 : APPLICANT: DUPRAT, FABRICE
 : APPLICANT: LESAGE, FLORIAN
 : APPLICANT: PINK, MICHEL
 : APPLICANT: SALINAS, MICHEL
 : APPLICANT: FARMAN, NICOLETTE
 : APPLICANT: LAZDUNSKI, MICHEL
 : TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR
 : TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF
 : TITLE OF INVENTION: DRUGS

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FILE REFERENCE: 1201-CIP2-00
CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/107,692
PRIOR FILING DATE: 1996-11-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 5
LENGTH: 405
TYPE: PRT
ORGANISM: Murine sp.
FEATURE:
OTHER INFORMATION: TASK
US-09-436-265-5

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Query Match      89.1%; Score 1819; DB 18; Length 405;
Best Local Similarity 88.1%; Pred. No. 7,6e-175;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

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QY 4 QNVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 63
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Db 1 ENVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 60
QY 64 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 123
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 120
QY 124 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 183
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 180
QY 184 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 243
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 240
QY 244 LRMTMNAEDEKRDARHALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 291
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LRMTMNAEDEKRDARHALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 290
QY 292 --GGGGRNVYAEVLHFGSMCSCLMYKSREKLOYSIPIIIPRDLSTSDTCVESHSSPG 349
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 GVGSGFRNVYAEVLHFGSMCSCLMYKSREKLOYSIPIIIPRDLSTSDTCVESHSSPG 360
QY 350 GGRYSDTPSPHCLSGTORSATSSVSTGLHSLSTFRGLMKRRSSV 394
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Db 361 GGRYSDTPSPHCLSGTORSATSSVSTGLHSLSTFRGLMKRRSSV 405

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RESULT 7
US-08-816-011C-55
Sequence 55, Application US/08816011C
GENERAL INFORMATION:
APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
FILE REFERENCE: 01142, 0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816, 011C
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332, 312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 55
LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
US-08-816-011C-55

```

```

QY 4 QNVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ENVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 60
QY 64 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 123
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 120
QY 124 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 183
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 180
QY 184 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 243
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 240
QY 244 LRMTMNAEDEKRDARHALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 291
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LRMTMNAEDEKRDARHALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 290
QY 292 --GGGGRNVYAEVLHFGSMCSCLMYKSREKLOYSIPIIIPRDLSTSDTCVESHSSPG 349
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 GVGSGFRNVYAEVLHFGSMCSCLMYKSREKLOYSIPIIIPRDLSTSDTCVESHSSPG 360
QY 350 GGRYSDTPSPHCLSGTORSATSSVSTGLHSLSTFRGLMKRRSSV 394
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 GGRYSDTPSPHCLSGTORSATSSVSTGLHSLSTFRGLMKRRSSV 405

```

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Query Match      60.5%; Score 1235.5; DB 12; Length 309;
Best Local Similarity 83.9%; Pred. No. 6.7e-116;
Matches 250; Conservative 8; Mismatches 27; Indels 13; Gaps 3;

```

```

QY 4 QNVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 13 ENVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 72
QY 64 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 123
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 132
QY 124 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 183
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 192
QY 184 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 241
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 249
QY 242 VVLRMTMNAEDEKRDARHALLTRNGQAGGGG-----GSAHTTDTASSTAAA 291
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 250 VVLRMTMNAEDEKRDARHALLTRNGQAGGGG-----GSAHTTDTASSTAAA 307

```

```

RESULT 8
US-08-816-011C-62
Sequence 62, Application US/08816011C
GENERAL INFORMATION:
APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
FILE REFERENCE: 01142, 0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816, 011C
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332, 312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 62
LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
US-08-816-011C-62

```

```

QY 4 QNVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 13 ENVRTALIVCTFTYLLVGAAVFDALSEPELIERORLELRQDELRLARYNLSSGGYEEL 72
QY 64 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 123
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 RVLRLKPKKAGVQWRFAGSFYFAITVITTTIGYHAAPSTDGKVCMEFYALLGIPLTLY 132
QY 124 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 183
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 MPOSIGERINTLVRLYLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSHEH 192
QY 184 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 241
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYIITGLTVIGAFPLNV 249
QY 242 VVLRMTMNAEDEKRDARHALLTRNGQAGGGG-----GSAHTTDTASSTAAA 291
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 250 VLVLFMTNNADEKRDADHRAHLLTHNGOAVGLGSLGSLGSGVPRDPVTCAAA 307

RESULT 9

US-08-816-011-55

; Sequence 55, Application US/08816011

; GENERAL INFORMATION:

; APPLICANT: Price, Laura A.

; APPLICANT: Pausch, Mark H.

; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences

; TITLE OF INVENTION: Encoding Them, and Methods of Using Same

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Home Products Corporation

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/816,011

; FILING DATE: 11-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Matthews, Gale F.

; REGISTRATION NUMBER: 32,269

; REFERENCE/DOCKET NUMBER: 32,421-C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2134

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 312 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-816-011-55

Query Match 59.9% Score 1224 DB 12 Length 312;

Best Local Similarity 83.1% Pred. No. 9.9e-115;

Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

Db 4 ONVRLALIVCTFTYLLVGAVPDALESEPELIERORLELRQOELRAVYNLSOGGYEEL 63

Db 13 ENVRTLALIVCTFTYLLVGAVPDALESEPEMIRORLELRQOELRAVYNLSOGGYEEL 72

Db 64 RVVRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDCGV--FCMFYALLGIP 120

Db 73 RVVRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDCGVFCMFYALLGIP 132

Db 121 TLVFOSLGERINTLVRLHRAKGLGMRADYMANMVLIGFSCISTLCIGAAFSH 180

Db 133 TLVFOSLGERINTSVRLHRAKGLGMRADYMANMVLIGFSCISTLCIGAAFSY 192

Db 181 YEHMTFOAYYYCFITLTITIGFDYVALQKDALOTOPQVYAFSFVYLLTGLTYIG--AF 238

Db 193 YEHMTFOAYYYCFITLTITIGFDYVALQKDALOTOPQVYAFSFVYLLTGLTYIG--AF 249

Db 239 LNLVLRFTMNADEKRDADHRAHLLTHNGOAVGLGSLGSLGSGVPRDPVTCAAA 290

Db 250 LNLVLRFTMNADEKRDADHRAHLLTHNGOAVGLGSLGSLGSGVPRDPVTCAAA 309

Db 291 A 291

Db 310 A 310

RESULT 10

US-08-816-011A-55

; Sequence 55, Application US/08816011A

; GENERAL INFORMATION:

; APPLICANT: Price, Laura A.

; APPLICANT: Pausch, Mark H.

; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences

; TITLE OF INVENTION: Encoding Them, and Methods of Using Same

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Home Products Corporation

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/816,011A

; FILING DATE: 11-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Matthews, Gale F.

; REGISTRATION NUMBER: 32,269

; REFERENCE/DOCKET NUMBER: 32,421-C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2134

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 312 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-816-011A-55

Query Match 59.9% Score 1224 DB 12 Length 312;

Best Local Similarity 83.1% Pred. No. 9.9e-115;

Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

Db 4 ONVRLALIVCTFTYLLVGAVPDALESEPELIERORLELRQOELRAVYNLSOGGYEEL 63

Db 13 ENVRTLALIVCTFTYLLVGAVPDALESEPEMIRORLELRQOELRAVYNLSOGGYEEL 72

Db 64 RVVRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDCGV--FCMFYALLGIP 120

Db 73 RVVRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDCGVFCMFYALLGIP 132

Db 121 TLVFOSLGERINTLVRLHRAKGLGMRADYMANMVLIGFSCISTLCIGAAFSH 180

Db 133 TLVFOSLGERINTSVRLHRAKGLGMRADYMANMVLIGFSCISTLCIGAAFSY 192

Db 181 YEHMTFOAYYYCFITLTITIGFDYVALQKDALOTOPQVYAFSFVYLLTGLTYIG--AF 238

Db 193 YEHMTFOAYYYCFITLTITIGFDYVALQKDALOTOPQVYAFSFVYLLTGLTYIG--AF 249

Db 239 LNLVLRFTMNADEKRDADHRAHLLTHNGOAVGLGSLGSLGSGVPRDPVTCAAA 290

Db 250 LNLVLRFTMNADEKRDADHRAHLLTHNGOAVGLGSLGSLGSGVPRDPVTCAAA 309

Db 291 A 291

Db 310 A 310

RESULT 11

US-09-516-279-2

; Sequence 2, Application US/09516279

```

: GENERAL INFORMATION:
: APPLICANT: David M. Duckworth
: APPLICANT: Robert J. Godden
: APPLICANT: Conrad G. Chapman
: APPLICANT: Helen J. Meadows
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30200
: CURRENT APPLICATION NUMBER: US/09/516,279
: CURRENT FILING DATE: 2000-03-01
: EARLIER APPLICATION NUMBER: UK 9905061.9
: EARLIER FILING DATE: 1999-03-05
: EARLIER APPLICATION NUMBER: UK 0003112.0
: EARLIER FILING DATE: 2000-02-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 374
: TYPE: PRF
: ORGANISM: HOMO SAPIENS
:
US-09-516-279-2

```

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Query Match Summary          54.7%: Score 1116: DB 19: Length 374:
Best Local Similarity       59.0%: Pred. No. 1.1e-103:
Matches 233: Conservative 44: Mismatches 96: Indels 22: Gaps 5

QY 1 MKRONVRLALVCTFTYLLVGAAYFDALSEPELIERORLELROELRARYNLSOGYE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKRONVRLTSLVCTFTYLLVGAAYFDALSEPEHEEREKLEAEFIRIKGTNISEDYR 60
QY 61 ELERVLLKPKKACVORNFAGSEFALTIVTTTIGYGAAPSTDGDKVCMETALLGTP 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 QELVTLQSEPRACVQMKFAGSEFALTIVTTTIGYGAAPSTDGKACMPEYAVIGPL 120
QY 121 TLVQMSLGERINTLVARLLHRAKGLGMRADVSMANVLLIGFESCISTLCIGAAAFSH 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 TLVQMSLGERINTLVARLLKRIKCCGMRNDVSEMMENVTVGFSCMKTLCIGAAAFSG 180
QY 181 YEHMTFPOAYYCFITLTGFGDYVALQKDALQTOPOYVAFSEVYILTLGTVIGAFNL 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 CEEMFSEHAYYCFITLTGFGDYVALQTKALOKKPLXYAFSEVYILTLGTVIGAFNL 240
QY 241 LVVLSEFMNMNDEKRDDEHRLALLRNQAGGGGGGSHHTDTPASSSTAAGGGERNY 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 LVVLSEFTLMSNDEKRDDEKRASTL-----AQRNSMVIHIPEEPPS-----RPXY 286
QY 301 -AEVLFPMQSCSLYKKREKLOYISIPMLPDLTSDPTVCQSHSPGCGGRYSPTPSR 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 287 KADVDLDQSVCSCTCYRRQD---YGRSVAAPNPSAKLAHPHFHSISKIEIISPSTLK 343
QY 360 RCLCSGAPRPAISVSYGLHSLSTFRGLMKRRSSV 394
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 344 NSLFP-----SPISSTSPGLHSPTDHRQLMKRRKSV 374

RESULT 12
US-09-516-279-4
; Sequence 4, Application US/09516279
; GENERAL INFORMATION:
; APPLICANT: David M. Duckworth
; APPLICANT: Robert J. Godden
; APPLICANT: Conrad G. Chapman
; APPLICANT: Helen J. Meadows
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30200
; CURRENT APPLICATION NUMBER: US/09/516,279
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: UK 9905061.9
; EARLIER FILING DATE: 1999-03-05
; EARLIER APPLICATION NUMBER: UK 0003112.0
; EARLIER FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 4
; LENGTH: 374
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-516-279-4

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	Query Match	Best Local Similarity	54.7%;	Score 116;	Di 1%;	Length 374;	
	Matches	233;	Conservative	44;	Mismatches	91;	
					Indels	22;	
					Gaps	5	
QY	1	MKRONVRLALIVCTFTYLLVGAALVDAL	SEPELIERORL	..KQELRARNL	NSOGGYE	60	
Db	1	MKRONVRLSLIVCTFTYLLVGAALVDAL	SEDHENREKEELVAEELIRKGNISSEDER			60	
QY	61	ELERVYLLPKKACVORFAGSEFEATVTVT	ITTYGYAAR	..S1DGGKVC	CMYALGIDPL	120	
Db	61	QLELVYLLSEPIRAVQMKFAGSEFEATVTVT	ITTYGYAAR	..P1DGGKVC	CMYAYVIGIDPL	120	
QY	121	TLVVFOSLGERINTLVARLLIHAKKGLG	MRADVSMANVLL	..GPFSCISTLC	IGAAAFSH	180	
Db	121	TLVVFOSLGERINTEFVRYLLKRIKCCG	RNRNDVEMEN	..VTVGCFPS	CMGTLCIGAAAFSG	180	
QY	181	YEHWFEOAYYYCFFTLTTLTGFGDYVAL	OKDALOTOP	..VAFSFY	YIITGLTVIGAFIN	240	
Db	181	CEEMFEFAYYYCFFTLTTLTGFGDYVAL	OKDALOKRPI	..VAFSFM	YIITGLTVIGAFIN	240	
QY	241	LVVLEFMTMAAEDERDAEHRALLTR	NRNOAGGGGGG	SAHITDTFAS	STAAGG	GFRRNY	300
Db	241	LVVLEFMTMAAEDERDAEHRALLTR	NRNOAGGGGGG	SAHITDTFAS	STAAGG	GFRRNY	300
QY	301	AEVLHFDSMCSCLMYKSKREKIQISIT	PMIIPDLSTSDT	..VLQSHSS	PEGGGRYS	SDTPSR	359
Db	287	KADVPDLQSVCSCTCTRSOD---	YCGRSVAPDNPSAKLA	PIHYFHSI	YKIEEIS	PSLTK	343
QY	360	RCLCGAPRASAISVSTGLHSLSTFRG	MLKRRSSV				394
Db	344	NSLFP---	SPISSTSPGLHSTFDHQR	LMKRRKSV			374

```

RESULT 13
US-60-199-020-2
: Sequence 2, Application US/60199020
: GENERAL INFORMATION:
: APPLICANT: Sanjanwala, Madhu Sudan
: APPLICANT: Baughn, Mariah R.
: APPLICANT: Yao, Monique G.
: APPLICANT: Nguyen, Daniel B.
: TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
: FILE REFERENCE: PI-0073 P
: CURRENT APPLICATION NUMBER: US/60/199,020
: CURRENT FILING DATE: 2000-04-20
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PERL Program
: SEQ ID NO 2
: LENGTH: 374
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 7472584CD1
US-60-199-020-2

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	Query Match	Similarity	Score	DB	Length
Best	Local	59.08%	59.08	1.1e-05	374
Matches	233	Conservative	44	Mismatches	22
				Indels	5
				Gaps	5

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:11:45 ; Search time 24.66 Seconds
(without alignments)
342.699 Million cell updates/sec

Title: US-09-503-089a-5
Perfect score: 2042
Sequence: 1 MKRONVRLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 154674 seqs, 21449152 residues

Total number of hits satisfying chosen parameters: 154674

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2042	100.0	394	5	US-09-798-584-15 Sequence 15, Appl
2	1278	62.6	238	5	US-09-746-491-61 Sequence 61, Appl
3	1116	54.7	374	5	US-09-798-584-1 Sequence 1, Appl
4	1069.5	52.4	365	5	US-09-746-491-60 Sequence 60, Appl
5	846	41.4	330	5	US-09-746-491-59 Sequence 59, Appl
6	838	41.0	330	5	US-09-746-491-58 Sequence 58, Appl
7	838	41.0	330	5	US-09-746-491-22 Sequence 22, Appl
8	363	17.8	411	5	US-09-336-643-83 Sequence 83, Appl
9	319	15.6	499	5	US-09-431-367B-2 Sequence 2, Appl
10	295.5	14.5	313	5	US-09-431-367B-8 Sequence 8, Appl
11	295.5	14.5	313	5	US-09-336-643-81 Sequence 81, Appl
12	294.5	14.4	332	5	US-09-431-367B-5 Sequence 11, Appl
13	251.5	12.3	401	5	US-09-431-367B-11 Sequence 11, Appl
14	179	8.8	39	5	US-09-746-491-63 Sequence 63, Appl
15	135.5	6.6	205	5	US-09-760-469-1386 Sequence 1386, Ap
16	131.5	6.4	646	5	US-09-336-643-10 Sequence 10, Appl
17	118	5.8	988	6	US-60-299-378-3 Sequence 3, Appl
18	118	5.8	988	6	US-60-300-614-3 Sequence 3, Appl
19	114	5.6	988	6	US-60-299-378-2 Sequence 2, Appl
20	114	5.6	988	6	US-60-300-614-2 Sequence 2, Appl
21	113.5	5.6	962	6	US-60-299-378-5 Sequence 5, Appl
22	113.5	5.6	962	6	US-60-300-614-5 Sequence 5, Appl
23	113.5	5.6	989	6	US-60-299-378-6 Sequence 6, Appl
24	113.5	5.6	989	6	US-60-300-614-6 Sequence 6, Appl
25	113	5.5	197	5	US-09-336-643-16 Sequence 16, Appl
26	112.5	5.5	1082	5	US-09-336-643-20 Sequence 20, Appl
27	111.5	5.5	962	6	US-60-299-378-4 Sequence 4, Appl

28	111.5	5.5	962	6	US-60-300-614-4 Sequence 4, Appl
29	111	5.4	947	6	US-60-304-243-2 Sequence 2, Appl
30	111	5.4	994	6	US-60-304-243-8 Sequence 8, Appl
31	103.5	5.1	950	6	US-60-304-243-9 Sequence 9, Appl
32	102.5	5.0	221	6	US-60-299-378-2 Sequence 21, Appl
33	102.5	5.0	221	6	US-60-300-614-2 Sequence 21, Appl
34	98.5	4.8	200	5	US-09-760-469-1 Sequence 1063, Ap
35	98.5	4.8	221	5	US-09-760-469-1 Sequence 1558, Ap
36	98.5	4.8	222	1	PCT-US01-18569- Sequence 1268, Ap
37	98.5	4.8	844	5	US-09-573-655A- Sequence 7, Appl
38	98.5	4.8	1174	6	US-60-299-378-7 Sequence 7, Appl
39	98.5	4.8	1174	6	US-60-300-614-7 Sequence 14, Appl
40	97.5	4.8	289	5	US-09-372-422A- Sequence 10, Appl
41	97.5	4.8	1195	6	US-60-304-243-4 Sequence 8, Appl
42	95.5	4.7	282	5	US-09-372-422A- Sequence 12, Appl
43	95.5	4.7	288	5	US-09-372-422A- Sequence 6, Appl
44	94	4.6	254	6	US-60-304-243-4 Sequence 49, Appl
45	94	4.6	1159	6	US-60-299-378-4

ALIGNMENTS

RESULT 1
US-09-798-584-15
; Sequence 15, Application US/09798584
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Talarik Inc.
; TITLE OF INVENTION: KCNB: A Novel Potassium
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; PRIOR FILING DATE: 2001-03-03
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human potassium channel K (TASK1)
US-09-798-584-15

us-09-503-089a-5

Query Match	100.0%	Score 2042	Length 394
Best local similarity	100.0%	Pred. No. 1	
Matches 394	Conservative 0	Mismatches	Indels 0
0		Gaps	0
OY	1	MKRONVRLALIVCTFTYLLVGAAVFDALRESEPLIEW	LRQELRAVYNLSGGYE 60
DB	1	MKRONVRLALIVCTFTYLLVGAAVFDALRESEPLIEW	LRQELRAVYNLSGGYE 60
OY	61	ELEEVNRLKPKHKGVMRFAGSFYFAITVTTTGYG	LDGGVFCMFYALGPI 120
DB	61	ELEEVNRLKPKHKGVMRFAGSFYFAITVTTTGYG	LDGGVFCMFYALGPI 120
OY	121	TLVFOGSLGERINTLVRYLHRAKKGJMRADYSMAH	GFSCISITLIGAAFSH 180
DB	121	TLVFOGSLGERINTLVRYLHRAKKGJMRADYSMAH	GFSCISITLIGAAFSH 180
OY	181	YEHHTFOAYVYCTITTTTGFGDYVALQDOALOTOP	GFSCISITLIGAAFSH 180
DB	181	YEHHTFOAYVYCTITTTTGFGDYVALQDOALOTOP	GFSCISITLIGAAFSH 180
OY	241	LVVLRFTMAEDERKRAEHRALLTRNGOAGGGGGG	GFSCISITLIGAAFSH 180
DB	241	LVVLRFTMAEDERKRAEHRALLTRNGOAGGGGGG	GFSCISITLIGAAFSH 180
OY	301	AEVLHFOGSLKMYKREKLYSIPMIIPDLSTST	GFSCISITLIGAAFSH 180
DB	301	AEVLHFOGSLKMYKREKLYSIPMIIPDLSTST	GFSCISITLIGAAFSH 180

Db 301 AEVLHQMCSCLMYSREKLOYISIMPIIPDLSTSDTCVESHSPGGGGRYSDTPSR 360
 QY 361 CLCGAPRSAISSVSTGLSHLSTFRGLMKRRSSV 394
 Db 361 CLCGAPRSAISSVSTGLSHLSTFRGLMKRRSSV 394

RESULT 2
 US-09-746-491-61
 ; Sequence 61, Application US/09746491
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgess, Catherine E.
 ; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-621
 ; CURRENT APPLICATION NUMBER: US/09/746,491
 ; CURRENT FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: USSN 60/171,329
 ; PRIOR FILING DATE: 1999-12-21
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 61
 ; LENGTH: 258
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-746-491-61

Query Match 62.6%; Score 1278; DB 5; Length 258;
 Best Local Similarity 96.1%; Pred. No. 5 8e-108;
 Matches 248; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAANFADALESEBELIEROLELROELRARNYLSGGYE 60
 Db 1 MKRONVRLALIVCTFTYLLVGAANFADALESEBELIEROLELROELRARNYLSGGYE 60
 QY 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120
 Db 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120
 QY 121 TLVMSLSGERINTLVRYLLHRAKGLGMRADVSMAVNYLIGFSCISTLCIGAASFH 180
 Db 121 TLVMSLSGERINTLVRYLLHRAKGLGMRADVSMAVNYLIGFSCISTLCIGAASFH 180
 QY 181 YEHMTFFQAYVYCFTLTITIGFDYVALOKDQALQTPQYVAFSEFYILTGLTVIGAFIN 240
 Db 181 YEHMTFFQAYVYCFTLTITIGFDYVALOKDQALQTPQYVAFSEFYILTGLTVIGAFIN 240
 QY 241 LVLRPMTNNADEKRD 258
 Db 241 LVLRPMTNNADEKRD 258

RESULT 3
 US-09-798-584-1
 ; Sequence 1, Application US/09798584
 ; GENERAL INFORMATION:
 ; APPLICANT: Mu, David
 ; APPLICANT: Powers, Scott
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: A Novel Potassium Channel Protein
 ; FILE REFERENCE: 018781-004010US
 ; CURRENT APPLICATION NUMBER: US/09/798,584
 ; CURRENT FILING DATE: 2001-03-03
 ; PRIOR APPLICATION NUMBER: US 60/186,951
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)

US-09-798-584-1

Query Match 54.7%; Score 1116; DB 5; Length 374;
 Best Local Similarity 59.0%; Pred. No. 3 9e-93;
 Matches 233; Conservative 44; Mismatches 9; Indels 22; Gaps 5;

QY 1 MKRONVRLALIVCTFTYLLVGAANFADALESEBELIEROLELROELRARNYLSGGYE 60
 Db 1 MKRONVRLALIVCTFTYLLVGAANFADALESEBELIEROLELROELRARNYLSGGYE 60
 QY 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120
 Db 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120
 QY 121 TLVMSLSGERINTLVRYLLHRAKGLGMRADVSMAVNYLIGFSCISTLCIGAASFH 180
 Db 121 TLVMSLSGERINTLVRYLLHRAKGLGMRADVSMAVNYLIGFSCISTLCIGAASFH 180
 QY 181 YEHMTFFQAYVYCFTLTITIGFDYVALOKDQALQTPQYVAFSEFYILTGLTVIGAFIN 240
 Db 181 YEHMTFFQAYVYCFTLTITIGFDYVALOKDQALQTPQYVAFSEFYILTGLTVIGAFIN 240
 QY 241 LVLRPMTNNADEKRDALTRNGAAGGGGSA :TASSTAAGGGGRNVY 300
 Db 241 LVLRPMTNNADEKRDALTRNGAAGGGGSA :TASSTAAGGGGRNVY 300
 QY 301 -AEVLHQMCSCLMYSREKLOYISIMPIIPDLSTSDTCVESHSPGGGGRYSDTPSR 359
 Db 287 KADVPDQSCVCTCYRSD---YGRSAVAPONSASAKLAPYFHSITKIEIISPTLK 343
 QY 360 KCLCGAPRSAISSVSTGLSHLSTFRGLMKRRSSV 394
 Db 344 NSLFP---SPISISPGHSTFDHQLMKRRKSV 374

RESULT 4
 US-09-746-491-60
 ; Sequence 60, Application US/09746491
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgess, Catherine E.
 ; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-621
 ; CURRENT APPLICATION NUMBER: US/09/746,491
 ; CURRENT FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: USSN 60/171,329
 ; PRIOR FILING DATE: 1999-12-21
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 60
 ; LENGTH: 365
 ; TYPE: PRT
 ; ORGANISM: Cavia porcellus
 US-09-746-491-60

Query Match 52.4%; Score 1069.5; DB 5; Length 365;
 Best Local Similarity 57.1%; Pred. No. 6e-84;
 Matches 226; Conservative 43; Mismatches 9; Indels 33; Gaps 6;

QY 1 MKRONVRLALIVCTFTYLLVGAANFADALESEBELIEROLELROELRARNYLSGGYE 60
 Db 1 MKRONVRLALIVCTFTYLLVGAANFADALESEBELIEROLELROELRARNYLSGGYE 60
 QY 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120
 Db 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120
 QY 121 TLVMSLSGERINTLVRYLLHRAKGLGMRADVSMAVNYLIGFSCISTLCIGAASFH 180
 Db 121 TLVMSLSGERINTLVRYLLHRAKGLGMRADVSMAVNYLIGFSCISTLCIGAASFH 180
 QY 181 YEHMTFFQAYVYCFTLTITIGFDYVALOKDQALQTPQYVAFSEFYILTGLTVIGAFIN 240
 Db 181 YEHMTFFQAYVYCFTLTITIGFDYVALOKDQALQTPQYVAFSEFYILTGLTVIGAFIN 240

Db 187 VPVAFPAHLEANSFLDAFYCFISLSTIGLDVYPGE----APGOPYRALYKVLVTVYL 242

Qy 229 LTGLT---VIGAFNLVLRMT-----MNAEDEKR 256

Db 243 FLGLVAMVLVLOTFRHVSDDLGLTLLPPCPASFADEDDR 286

RESULT 11

US-09-336-643-81

Sequence 81, Application US/09336643

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Curran, Mark Edward

APPLICANT: Hu, Ping

APPLICANT: Rutter, Marc

APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: Novel Human Potassium Channels

FILE REFERENCE: SEQ-15P

CURRENT APPLICATION NUMBER: US/09/336,643

CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR FILING DATE: 1998-08-07

PRIOR APPLICATION NUMBER: 60/116,448

PRIOR FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: PCT/US99/03826

PRIOR FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 81

LENGTH: 313

TYPE: PRT

ORGANISM: H. sapiens

US-09-336-643-81

Query Match 14.5%; Score 295.5; DB 5; Length 313;

Best Local Similarity 31.7%; Pred. No. 3,7e-19;

Matches 90; Conservative 40; Mismatches 95; Indels 59; Gaps 12;

Qy 18 YLVGAANFDLSEPELIERORLELROQLRARN-----LSGGYELE 63

Db 17 YLVGALLVLRLEGPHRELRLELETLRAQLQSPCYAARALDAFVERVLAAG---RLG 73

Qy 64 RVLRLKPKHKAQV---WRFAGSEFYATVTTTIGYGAAPSTDGKVFCEFYALLGIP 120

Db 74 RVLANAGSGANASDPAMDPAFSALEFASTLITVGYGTTPLTDGAKFSAIFALLGVP 133

Qy 121 TLVWFOSIGERINTLVRLYLRKAKGIGM-----RRADVSMAWNLIGFSCISTLC-- 172

Db 134 TMLLTASAQRSLT---LTHVPLSLMSRMGMDPRRA---ACWHLVALLGVVTVCF 186

Qy 173 IGAASFVHEH-WTFQAYVYCFITLTITIGFDVVALOKDQALQTPQ---YVAFSPYI 228

Db 187 VPVAFPAHLEANSFLDAFYCFISLSTIGLDVYPGE---APGOPYRALYKVLVTVYL 242

Qy 229 LTGLT---VIGAFNLVLRMT-----MNAEDEKR 256

Db 243 FLGLVAMVLVLOTFRHVSDDLGLTLLPPCPASFADEDDR 286

RESULT 12

US-09-431-367B-5

Sequence 5, Application US/09431367B

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: NMI-074CP

CURRENT APPLICATION NUMBER: US/09/431,367B

CURRENT FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 09/259,951

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 332

TYPE: PRT

ORGANISM: Homo sapiens

US-09-431-367B-5

Query Match 14.4%; Score 294.5; DB 5; Length 332;

Best Local Similarity 29.9%; Pred. No. 4.9e-15;

Matches 76; Conservative 52; Mismatches 19; Indels 19; Gaps 6;

Qy 8 TLALVCTFTYLLVGAANFDLSEPELIERORLELRK---ARYN-LSGGYELEERV 66

Db 22 TVLLLLVLAVALGVTGFWTLEGRAQDSSRSRQDR---JNFTCDPRALDSLIRDV 81

Qy 67 LRLPKHKAQV-----QWRFAGSEFYATVTTTIGYGAAPSTDGKVFCEFYALLGIP 118

Db 82 VQAYKNGASLLSNTSMGRMELVGSFFSVSTITITIGYGAAPSTDGKVFCEFYALLGIP 141

Qy 119 PLTVWFOSIGERINTLVRLYLRKAKGIGMRADVSMT---TIGFSCIS---TLCIG 174

Db 142 PLNLVLRNRLGHLMQGVNHHASR---LGGTMDPQKAKH-LAGSGLLSGLLPLILP 196

Qy 175 AAASFVHEH-WTFQAYVYCFITLTITIGFDVVALOKDQALQTPQ---YVAFSPYI 234

Db 197 PLFESHMGMSYTGFEYAFITLSTVGGDYV-IGMNPSCQ---YVAFSPYI 255

Qy 235 IGAFLNLVLRMT 248

Db 256 LALIKILLSQLET 269

RESULT 13

US-09-431-367B-11

Sequence 11, Application US/09431367B

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: NMI-074CP

CURRENT APPLICATION NUMBER: US/09/431,367B

CURRENT FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 09/259,951

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11

LENGTH: 401

TYPE: PRT

ORGANISM: Homo sapiens

US-09-431-367B-11

Query Match 12.3%; Score 251.5; DB 5; Length 401;

Best Local Similarity 22.9%; Pred. No. 4.7e-15;

Matches 81; Conservative 39; Mismatches 19; Indels 129; Gaps 8;

Qy 9 LALVCTFTYLLVGAANFDLSEPELIERORLELRK---ARYN-LSGGYELEERV 62

Db 41 LCFICFLVTVLAVGAVVSALIEDGOVLAADGDEFKEL---RLNCSFVEVDEBRKODL 100

Qy 63 ERVYLRLKPKH--KAGVQWRFAGSEFYATVTTTIGYGAAPSTDGKVFCEFYALLGIP 120

Db 101 OGHLQKVKAPQWENRTTHMSFLSLFECCTVSTVGYG---FLRGYLCMLYALFGIPL 160

Qy 121 TLVWFOSIGERINTLVRLYLRKAKGIGM-----RRADVSMAWNLIGFSCISTLC-- 172

Db 161 MFLVLTDTGDLATLITSTYNRFRKFPFTPLRLSKWCP---KKKPKPADPAVPOII 220

Qy 146 ----- 145

Db 221 ISAEELPQPKIGTCSRSCSMELFERSHALEKONTLOI---AMRSNCEPLVIGRLSY 280

Qy 146 ----- 193

DB 281 SIISNDEVOQOVERLIDIPITIALIVFAYISC-----AAALPEWETOLDPENAFYFC 334
OY 194 FITLTTIGFGDYVALQDQALQTOPOVYAFVYLLGLVIGAFNLVYLFREM 247
DB 335 FVLLTTIGFGDYVL-----EHPNFFLFSTIYIGMEIVFAFKLVONRLI 380

Search completed: August 28, 2001, 17:11:45
Job time: 389 sec

RESULT 14
US-09-746-491-63
; Sequence 63, Application US/09746491
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-746-491-63

Query Match 8.8%; Score 179; DB 5; Length 39;
Best Local Similarity 87.2%; Pred. No. 8.9e-10;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 338 TCVEQSHSPGGGGRYSDTPSRRLCSGAPRSATSSYST 376
DB 1 TCVEHSHSPGGGGRYSDTPSRRLCSGATQRSATSSYST 39

RESULT 15
US-09-760-469-1386
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1386
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1386

Query Match 6.6%; Score 135.5; DB 5; Length 205;
Best Local Similarity 34.4%; Pred. No. 6e-05;
Matches 43; Conservative 17; Mismatches 48; Indels 17; Gaps 5;

OY 148 GMRADVSMANMVLIGFFSCITLIGAAAFSHYE-HMFFQAYVYCFITLTTIGFGDYV 206
DB 42 GFESKQYVAIVHAYLVGVVSCFFPIPAVAFSVLEDDWNFLSFYCFITSLSTIGLDYV 101
OY 207 A-----LQKDAQLOFOPQYVAFSFVYITG---LTVIGAFNLVVL---RFTMNADEK 255
DB 102 PGEGYQKFEREL-----YKIGITCYLLGLIAMLVLETFCEHLELKKFRKMFYVKKDKD 156
OY 256 RDAEH 260
DB 157 EDOVH 161

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:11:13 ; Search time 242.67 Seconds
(without alignments)
375.734 Million cell updates/sec

Title: US-09-503-089A-4

Perfect score: 2090
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Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2090	100.0	411	19	US-09-503-089A-4
2	2084	99.7	411	22	US-09-828-746-6
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4	2044	97.8	411	17	US-09-336-643-83
5	2044	97.8	411	17	US-09-336-643-83
6	2044	97.8	411	22	US-09-828-746-2
7	2041	97.7	411	19	US-09-503-089A-2
8	2011	96.2	426	12	US-08-816-011A-45
9	2011	96.2	426	12	US-08-816-011A-45
10	2011	96.2	426	12	US-08-816-011C-45

11	1864	89.2	370	20	US-09-655-272-4	Sequence 4, Appl
12	1855	88.8	370	15	US-09-144-914-8	Sequence 8, Appl
13	1855	88.8	370	18	US-09-436-265-8	Sequence 8, Appl
14	1251.5	59.9	543	1	PCT-US01-14965-7	Sequence 73, Appl
15	1251.5	59.9	543	22	US-09-852-386-7	Sequence 73, Appl
16	1250	59.8	657	23	US-60-207-583-3	Sequence 376, App
17	1224	58.6	724	23	US-60-216-547-1	Sequence 10, Appl
18	1207.5	57.8	484	23	US-60-230-445-16	Sequence 1632, Ap
19	797	38.1	392	1	PCT-US00-34983B-55	Sequence 55, Appl
20	797	38.1	392	21	US-09-729-739-5	Sequence 55, Appl
21	797	38.1	393	18	US-09-432-470-2	Sequence 2, Appl
22	797	38.1	393	18	US-09-432-470-4	Sequence 2, Appl
23	797	38.1	419	22	US-09-828-035-2	Sequence 2, Appl
24	797	38.1	440	23	US-60-258-275-4	Sequence 424, App
25	797	38.1	1314	1	PCT-US00-34983B-55	Sequence 29, Appl
26	797	38.1	1314	21	US-09-729-739-5	Sequence 29, Appl
27	770.5	36.9	398	20	US-09-655-272-2	Sequence 2, Appl
28	753.5	36.1	1779	23	US-60-212-358-1	Sequence 133, Appl
29	753.5	36.1	1785	23	US-60-207-416-9	Sequence 91, Appl
30	752	36.0	1616	23	US-60-229-525-3	Sequence 331, App
31	640.5	30.6	1068	23	US-60-212-358-1	Sequence 195, Appl
32	551	26.4	107	22	US-09-828-746-4	Sequence 4, Appl
33	510	24.4	295	23	US-60-223-269-8	Sequence 8, Appl
34	506	24.2	110	23	US-60-171-487-5	Sequence 594, App
35	420	20.1	499	16	US-09-259-951-2	Sequence 2, Appl
36	420	20.1	499	16	US-09-259-951-4	Sequence 4, Appl
37	420	20.1	499	17	US-09-357-425-1	Sequence 6, Appl
38	420	20.1	499	18	US-09-436-265-2	Sequence 28, Appl
39	420	20.1	499	19	US-09-561-763-2	Sequence 2, Appl
40	420	20.1	499	21	US-09-735-169-2	Sequence 2, Appl
41	420	20.1	499	21	US-09-735-169-4	Sequence 4, Appl
42	420	20.1	499	21	US-09-735-169A-4	Sequence 2, Appl
43	420	20.1	499	21	US-09-735-171-2	Sequence 2, Appl
44	420	20.1	499	21	US-09-735-171-4	Sequence 4, Appl
45	420	20.1	499	21	US-09-735-171A-4	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-503-089A-4
: Sequence 4, Application US/09503089A
: GENERAL INFORMATION:
: APPLICANT: PATEL, AMANDA J.
: APPLICANT: HONORE, ERIC
: APPLICANT: LESAGE, FLORIAN
: APPLICANT: ROMERY, GEORGES
: APPLICANT: LAZDUSKI, MICHEL
: TITLE OF INVENTION: A method for the identification of anesthetics
: FILE REFERENCE: f17b12pro3-humanantREK
: CURRENT APPLICATION NUMBER: US/09/503,089A
: CURRENT FILING DATE: 2000-02-11
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: Microsoft Word 2000
: SEQ ID NO 4
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-503-089A-4

Query Match 100.0%; Score 2090; DB 19; Length 411;
Best Local Similarity 100.0%; Pred. No. 5; Idels 0; Gaps 0;
Matches 411; Conservative 0; Mismatches 0;
QY 1 MAADPLDPKSAQNSKPR...LNGTTPHCAGEDIATVEMNK 411
DB 1 MAADPLDPKSAQNSKPR...LNGTTPHCAGEDIATVEMNK 411
QY 61 GAAVFALEDPQETISORTTIVIKOTFTIAQACVNSTELMELQIVAVINAGIIPLGNS 120
DB 61 GAAVFALEDPQETISORTTIVIKOTFTIAQACVNSTELMELQIVAVINAGIIPLGNS 120

```

OY 121 SNOVSHMDLGSFFPAGYITTTGFCNISPRTGKIFCIYALLGLPGLAGVGDQ 180
    |||||||
Db 121 SNOVSHMDLGSFFPAGYITTTGFCNISPRTGKIFCIYALLGLPGLAGVGDQ 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
OY 241 AITFVVITTTTIGFDYVAGSDIEYLDYKPPVWFMILVGLAFYAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AITFVVITTTTIGFDYVAGSDIEYLDYKPPVWFMILVGLAFYAAVLSMIGDMLRVIS 300
OY 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
OY 361 ELTPCRRITLSVNHLTSEREVLPPLKAESIYINGLTPHCAGEDIAVIENMK 411
    |||||||
Db 361 ELTPCRRITLSVNHLTSEREVLPPLKAESIYINGLTPHCAGEDIAVIENMK 411

```

RESULT 2

```

US-09-828-746-6
; Sequence 6, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-DI
; CURRENT APPLICATION NUMBER: US/09/828,746
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

```

Abv

Pre grant Pub.

20020028485

```

Query Match          99.7%; Score 2084; DB 22; Length 411;
Best Local Similarity 99.8%; Pred. No. 2.1e-203;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLI 60
    |||||||
Db 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLI 60
OY 61 GAAYFALBQPOEISORTTIVIOKOTFIQAHCANSTELDELIOQIVAAINAGIIPLGNS 120
    |||||||
Db 61 GAAYFALBQPOEISORTTIVIOKOTFIQAHCANSTELDELIOQIVAAINAGIIPLGNS 120
OY 121 SNOVSHMDLGSFFPAGYITTTGFCNISPRTGKIFCIYALLGLPGLAGVGDQ 180
    |||||||
Db 121 SNOVSHMDLGSFFPAGYITTTGFCNISPRTGKIFCIYALLGLPGLAGVGDQ 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
OY 241 AITFVVITTTTIGFDYVAGSDIEYLDYKPPVWFMILVGLAFYAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AITFVVITTTTIGFDYVAGSDIEYLDYKPPVWFMILVGLAFYAAVLSMIGDMLRVIS 300
OY 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360

```

```

Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
OY 361 ELTPCRRITLSVNHLTSEREVLPPLKAESIYINGLTPHCAGEDIAVIENMK 411
    |||||||
Db 361 ELTPCRRITLSVNHLTSEREVLPPLKAESIYINGLTPHCAGEDIAVIENMK 411

```

RESULT 3

```

PCT-US99-03826-83
; Sequence 83, Application PC/TUS9903826A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: NOVEL HUMAN POTASSIUM CHANNEL
; FILE REFERENCE: SEQ-15PCT
; CURRENT APPLICATION NUMBER: PCT/US99/03826A
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
PCT-US99-03826-83

```

```

Query Match          97.8%; Score 2044; DB 1; Length 411;
Best Local Similarity 96.4%; Pred. No. 2.6e-19;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLI 60
    |||||||
Db 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLI 60
OY 61 GAAYFALBQPOEISORTTIVIOKOTFIQAHCANSTELDELIOQIVAAINAGIIPLGNS 120
    |||||||
Db 61 GAAYFALBQPOEISORTTIVIOKOTFIQAHCANSTELDELIOQIVAAINAGIIPLGNS 120
OY 121 SNOVSHMDLGSFFPAGYITTTGFCNISPRTGKIFCIYALLGLPGLAGVGDQ 180
    |||||||
Db 121 SNOVSHMDLGSFFPAGYITTTGFCNISPRTGKIFCIYALLGLPGLAGVGDQ 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
OY 241 AITFVVITTTTIGFDYVAGSDIEYLDYKPPVWFMILVGLAFYAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AITFVVITTTTIGFDYVAGSDIEYLDYKPPVWFMILVGLAFYAAVLSMIGDMLRVIS 300
OY 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
OY 361 ELTPCRRITLSVNHLTSEREVLPPLKAESIYINGLTPHCAGEDIAVIENMK 411
    |||||||
Db 361 ELTPCRRITLSVNHLTSEREVLPPLKAESIYINGLTPHCAGEDIAVIENMK 411

```

RESULT 4

```

US-09-336-643-83
; Sequence 83, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; APPLICANT: Ping Hu
; APPLICANT: Marc Rutter

```

6,399,761


```

; APPLICANT: Jian-Ying Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; EARLIER FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: PCT/US99/03826
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

```

```

Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 2,6e-199;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDSAINVKKVSTFLVVLII 60
    |||
DB 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDPTINVMKKVSTFLVVLII 60
    |||
QY 61 GAATVFALEOPHEISQRTTVIOKQFIHACVNSTEDELIOQVAAINAGIIPGNS 120
    |||
DB 61 GAATVFALEOPHEISQRTTVIOKQFIHACVNSTEDELIOQVAAINAGIIPGNT 120
    |||
QY 121 SNOVSHDLSSFFAGTATTGFGNISPRTEGKIFCIITALLGIPFLAGVGDQ 180
    |||
DB 121 SNOVSHDLSSFFAGTATTGFGNISPRTEGKIFCIITALLGIPFLAGVGDQ 180
    |||
QY 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIFILFGCVLPAVPAVIRKHIEGMSALD 240
    |||
DB 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIFILFGCVLPAVPAVIRKHIEGMSALD 240
    |||
QY 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLFVIS 300
    |||
DB 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLFVIS 300
    |||
QY 301 KKTKEVEGEFRAHAEMTAVTAEFKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||
DB 301 KKTKEVEGEFRAHAEMTAVTAEFKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||
QY 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYLNGLTPHCAGEELAVIENIK 411
    |||
DB 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYLNGLTPHCAGEELAVIENIK 411
    |||

```

```

RESULT 5
US-09-336-643-83
; Sequence 83, Application US/09336643A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; EARLIER FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: PCT/US99/03826
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

```

```

Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 2,6e-199;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDSAINVKKVSTFLVVLII 60
    |||
DB 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDPTINVMKKVSTFLVVLII 60
    |||
QY 61 GAATVFALEOPHEISQRTTVIOKQFIHACVNSTEDELIOQVAAINAGIIPGNS 120
    |||
DB 61 GAATVFALEOPHEISQRTTVIOKQFIHACVNSTEDELIOQVAAINAGIIPGNT 120
    |||
QY 121 SNOVSHDLSSFFAGTATTGFGNISPRTEGKIFCIITALLGIPFLAGVGDQ 180
    |||
DB 121 SNOVSHDLSSFFAGTATTGFGNISPRTEGKIFCIITALLGIPFLAGVGDQ 180
    |||
QY 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIFILFGCVLPAVPAVIRKHIEGMSALD 240
    |||
DB 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIFILFGCVLPAVPAVIRKHIEGMSALD 240
    |||
QY 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLFVIS 300
    |||
DB 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLFVIS 300
    |||
QY 301 KKTKEVEGEFRAHAEMTAVTAEFKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||
DB 301 KKTKEVEGEFRAHAEMTAVTAEFKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||
QY 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYLNGLTPHCAGEELAVIENIK 411
    |||
DB 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYLNGLTPHCAGEELAVIENIK 411
    |||

```

```

RESULT 6
US-09-828-746-2
; Sequence 2, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; EARLIER FILING DATE: 2001-04-09
; EARLIER APPLICATION NUMBER: US/09/236,080
; EARLIER FILING DATE: 1999-01-25
; EARLIER APPLICATION NUMBER: EP 98300570.3
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: UK 9822135.1
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2

```

```

Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 2,6e-199;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDSAINVKKVSTFLVVLII 60
    |||
DB 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDPTINVMKKVSTFLVVLII 60
    |||

```

26020.28485
ABN

QY 61 GAAVEKALBOPBISORTTIVIOKOTFIQAHCVNSTELDELIOQIVAAINAGIPLGNS 120
DB 61 GAAVEKALBOPBISORTTIVIOKOTFIQAHCVNSTELDELIOQIVAAINAGIPLGNT 120
QY 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDQ 180
DB 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDQ 180
QY 181 LGTIFGKGLAKVEDTIFIKNNVSQTKIRIISTITIFLFGCVLPAVALPAVEFKHIEGMSALD 240
DB 181 LGTIFGKGLAKVEDTIFIKNNVSQTKIRIISTITIFLFGCVLPAVALPAVEFKHIEGMSALD 240
QY 241 AITFVYITTTIGFGDYVAGSGDIEYLDYKPPVWFMILVGLAFYAVLSMIGDMLRVIS 300
DB 241 AITFVYITTTIGFGDYVAGSGDIEYLDYKPPVWFMILVGLAFYAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360
DB 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360

RESULT 7

US-09-503-089a-2
Sequence 2, Application US/09503089A
GENERAL INFORMATION:
APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: LESAGE, FLORIAN
APPLICANT: ROMNEY, GEORGES
APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identification of anesthetics
FILE REFERENCE: f17b12p0v3-humantrek
CURRENT APPLICATION NUMBER: US/09/503,089A
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
SEQ ID NO 2
LENGTH: 411
TYPE: PRF
ORGANISM: Homo sapiens
US-09-503-089a-2

not out

Query Match 97.7%; Score 2041; DB 19; Length 411;
Best Local Similarity 96.1%; Pred. No. 5, 2e-199;
Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAAPDLDPKSAONSKPRLSFSSKPTVLAASRVESDITINVMKVTSTFLVVLXLI 60
DB 1 MAAPDLDPKSAONSKPRLSFSSKPTVLAASRVESDITINVMKVTSTFLVVLXLI 60
QY 61 GAAVEKALBOPBISORTTIVIOKOTFIQAHCVNSTELDELIOQIVAAINAGIPLGNS 120
DB 61 GAAVEKALBOPBISORTTIVIOKOTFIQAHCVNSTELDELIOQIVAAINAGIPLGNT 120
QY 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDQ 180
DB 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDQ 180
QY 181 LGTIFGKGLAKVEDTIFIKNNVSQTKIRIISTITIFLFGCVLPAVALPAVEFKHIEGMSALD 240
DB 181 LGTIFGKGLAKVEDTIFIKNNVSQTKIRIISTITIFLFGCVLPAVALPAVEFKHIEGMSALD 240
QY 241 AITFVYITTTIGFGDYVAGSGDIEYLDYKPPVWFMILVGLAFYAVLSMIGDMLRVIS 300
DB 241 AITFVYITTTIGFGDYVAGSGDIEYLDYKPPVWFMILVGLAFYAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360
DB 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360

DB 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360
QY 361 ELTPCRRILSVNHLNTERDVLPLLTSTIYNGLTPHCAEIAVENIK 411
DB 361 ELTPCRRILSVNHLNTERDVLPLLTSTIYNGLTPHCAEIAVENIK 411

RESULT 8

US-08-816-011-45
Sequence 45, Application US/08816011
GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
TITLE OF INVENTION: Encoding Them, and Methods of Using Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,421-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-4117
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-816-011-45

3/11/97

20030165806

Query Match 96.2%; Score 2011; DB 19; Length 426;
Best Local Similarity 95.1%; Pred. No. 6, 3e-199;
Matches 391; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAAPDLDPKSAONSKPRLSFSSKPTVLAASRVESDITINVMKVTSTFLVVLXLI 60
DB 1 MAAPDLDPKSAONSKPRLSFSSKPTVLAASRVESDITINVMKVTSTFLVVLXLI 60
QY 61 GAAVEKALBOPBISORTTIVIOKOTFIQAHCVNSTELDELIOQIVAAINAGIPLGNS 120
DB 61 GAAVEKALBOPBISORTTIVIOKOTFIQAHCVNSTELDELIOQIVAAINAGIPLGNT 120
QY 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDQ 180
DB 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDQ 180
QY 181 LGTIFGKGLAKVEDTIFIKNNVSQTKIRIISTITIFLFGCVLPAVALPAVEFKHIEGMSALD 240
DB 181 LGTIFGKGLAKVEDTIFIKNNVSQTKIRIISTITIFLFGCVLPAVALPAVEFKHIEGMSALD 240
QY 241 AITFVYITTTIGFGDYVAGSGDIEYLDYKPPVWFMILVGLAFYAVLSMIGDMLRVIS 300
DB 241 AITFVYITTTIGFGDYVAGSGDIEYLDYKPPVWFMILVGLAFYAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360
DB 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360

OY 301 KTKEEGEFRAHAAEWTANTATAEKTRRLRLSEIYDKFORATSVKRLSAELAGNHQ 360
DB 316 KTKEEGEFRAHAAEWTANTATAEKTRRLRLSEIYDKFORATSVKRLSAELAGNHQ 375
OY 361 ELTPCRRLSVNHLTSEREVLPPLKKAESIYNLNGTFCGEDIJAVIENMK 411
DB 376 ELTPCRRLSVNHLTSEREVLPPLKKAESIYNLNGTFCGEDIJAVIENMK 426

RESULT 9

US-08-816-011A-45
Sequence 45, Application US/08816011A
GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
TITLE OF INVENTION: Encoding Them, and Methods of Using Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816.011A
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,421-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-816-011A-45

Query Match 96.2%; Score 2011; DB 12; Length 426;
Best Local Similarity 95.1%; Pred. No. 6.3e-196;
Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDSAINVMKKTSTIFLVVLYLI 60
DB 16 VAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 75
OY 61 GAAVFKALEOPQISORTTIVIKOTFIQAHCYNSTELDELIOQIYAIAINAGIIPLGNS 120
DB 76 GAAVFKALEOPQISORTTIVIKOTFIQAHCYNSTELDELIOQIYAIAINAGIIPLGNT 135
OY 121 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITALLGIPLEFLLAGVGDQ 180
DB 136 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITALLGIPLEFLLAGVGDQ 195
OY 181 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIRKHEGMSALD 240
DB 196 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIRKHEGMSALD 255
OY 241 AIYFVVTLLTIGFGDVAGSDIEYLDYKPVVWFMLVGLAFAVLSMIGMLRVIS 300
DB 256 AIYFVVTLLTIGFGDVAGSDIEYLDYKPVVWFMLVGLAFAVLSMIGMLRVIS 315

OY 301 KTKEEGEFRAHAAEWTANTATAEKTRRLRLSEIYDKFORATSVKRLSAELAGNHQ 360
DB 316 KTKEEGEFRAHAAEWTANTATAEKTRRLRLSEIYDKFORATSVKRLSAELAGNHQ 375
OY 361 ELTPCRRLSVNHLTSEREVLPPLKKAESIYNLNGTFCGEDIJAVIENMK 411
DB 376 ELTPCRRLSVNHLTSEREVLPPLKKAESIYNLNGTFCGEDIJAVIENMK 426

RESULT 10

US-08-816-011C-45
Sequence 45, Application US/08816011C
GENERAL INFORMATION:
APPLICANT: Pausch, Mark H.
APPLICANT: Price, Laura A.
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 426
TYPE: PRT
ORGANISM: Homo sapiens
US-08-816-011C-45

Query Match 96.2%; Score 2011; Length 426;
Best Local Similarity 95.1%; Pred. No. 6.3e-196;
Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDSAINVMKKTSTIFLVVLYLI 60
DB 16 VAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 75
OY 61 GAAVFKALEOPQISORTTIVIKOTFIQAHCYNSTELDELIOQIYAIAINAGIIPLGNS 120
DB 76 GAAVFKALEOPQISORTTIVIKOTFIQAHCYNSTELDELIOQIYAIAINAGIIPLGNT 135
OY 121 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITALLGIPLEFLLAGVGDQ 180
DB 136 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITALLGIPLEFLLAGVGDQ 195
OY 181 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIRKHEGMSALD 240
DB 196 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIRKHEGMSALD 255
OY 241 AIYFVVTLLTIGFGDVAGSDIEYLDYKPVVWFMLVGLAFAVLSMIGMLRVIS 300
DB 256 AIYFVVTLLTIGFGDVAGSDIEYLDYKPVVWFMLVGLAFAVLSMIGMLRVIS 315
OY 301 KTKEEGEFRAHAAEWTANTATAEKTRRLRLSEIYDKFORATSVKRLSAELAGNHQ 360
DB 316 KTKEEGEFRAHAAEWTANTATAEKTRRLRLSEIYDKFORATSVKRLSAELAGNHQ 375
OY 361 ELTPCRRLSVNHLTSEREVLPPLKKAESIYNLNGTFCGEDIJAVIENMK 411
DB 376 ELTPCRRLSVNHLTSEREVLPPLKKAESIYNLNGTFCGEDIJAVIENMK 426

RESULT 11
US-09-655-272-4
Sequence 4, Application US/09655272
GENERAL INFORMATION:
APPLICANT: HONORE, ERIC
APPLICANT: FINK, MICHEL

```

; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: DUPRAT, FABRICE
; TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
; TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
; TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
; FILE REFERENCE: 1383-00
; CURRENT APPLICATION NUMBER: US/09/655,272
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/FR99/00404
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: FR 98/02725
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Unknown Sequence
; FEATURE:
; OTHER INFORMATION: Description of Unknown Sequence: TREK
US-09-655-272-4

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Query Match      89.2%; Score 1864; DB 20; Length 370;
Best Local Similarity 99.7%; Pred. No. 5,3e-181;
Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINWMTVSTFLVVLXLI 60
DB 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINWMTVSTFLVVLXLI 60
OY 61 GAAVFALBPOEISORTTIVIOKOTFIAOHACVNSTELDELOQIVAAINAGIPLGNS 120
DB 61 GAAVFALBPOEISORTTIVIOKOTFIAOHACVNSTELDELOQIVAAINAGIPLGNS 120
OY 121 SNOVSHMDLGSFFAGVYITTTGFGNISPRTEGKIFCTIYALLGIPLEGFLAGVGDO 180
DB 121 SNOVSHMDLGSFFAGVYITTTGFGNISPRTEGKIFCTIYALLGIPLEGFLAGVGDO 180
OY 121 SNOVSHMDLGSFFAGVYITTTGFGNISPRTEGKIFCTIYALLGIPLEGFLAGVGDO 180
DB 121 SNOVSHMDLGSFFAGVYITTTGFGNISPRTEGKIFCTIYALLGIPLEGFLAGVGDO 180
OY 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLPAVAVIFKHIEGMSALD 240
DB 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLPAVAVIFKHIEGMSALD 240
OY 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILVGLAYFAVLSMIGDWLRVIS 300
DB 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILVGLAYFAVLSMIGDWLRVIS 300
OY 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
DB 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
OY 361 ELTPCART 368
DB 361 ELTPCART 368

```

```

RESULT 12
US-09-144-914-8
; Sequence 8, Application US/09144914
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989,6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234

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; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-144-914-8

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Query Match      88.8%; Score 1855; DB 20; Length 370;
Best Local Similarity 99.5%; Pred. No. 4,4e-177;
Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINWMTVSTFLVVLXLI 60
DB 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINWMTVSTFLVVLXLI 60
OY 61 GAAVFALBPOEISORTTIVIOKOTFIAOHACVNSTELDELOQIVAAINAGIPLGNS 120
DB 61 GAAVFALBPOEISORTTIVIOKOTFIAOHACVNSTELDELOQIVAAINAGIPLGNS 120
OY 121 SNOVSHMDLGSFFAGVYITTTGFGNISPRTEGKIFCTIYALLGIPLEGFLAGVGDO 180
DB 121 SNOVSHMDLGSFFAGVYITTTGFGNISPRTEGKIFCTIYALLGIPLEGFLAGVGDO 180
OY 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLPAVAVIFKHIEGMSALD 240
DB 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLPAVAVIFKHIEGMSALD 240
OY 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILVGLAYFAVLSMIGDWLRVIS 300
DB 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILVGLAYFAVLSMIGDWLRVIS 300
OY 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
DB 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
OY 361 ELTPCART 368
DB 361 ELTPCART 368

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RESULT 13
US-09-436-265-8
; Sequence 8, Application US/09436265
; GENERAL INFORMATION:
; APPLICANT: REYES, ROBERTO
; APPLICANT: DUPRAT, FABRICE
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: FINK, MICHEL
; APPLICANT: SALINAS, MIGUEL
; APPLICANT: FARMAN, NICOLETTE
; APPLICANT: LAZDUNSKI, MICHEL
; TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR
; TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 1201-CIP2-00
; CURRENT APPLICATION NUMBER: US/09/436,265
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/107,692
; PRIOR FILING DATE: 1996-11-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT

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ORGANISM: Murine sp.
FEATURE:
OTHER INFORMATION: TREK-1
US-09-436-265-8

Query Match 88.8%; Score 1855; DB 18; Length 370;
Best Local Similarity 99.5%; Pred. No. 4,4e-180;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 MAADLLDPKSAONSKPRLSFSSKPPYLASRVSDSAINMKKKTSTIFLVVLYLI 60
D 1 MAADLLDPKSAONSKPRLSFSSKPPYLASRVSDSAINMKKKTSTIFLVVLYLI 60
Y 61 GAAVFAKLEQPOEISQRTTIVIOKOTFIAQACVNSTELDELIOQIYVAIINAGIIPGNS 120
D 61 GAAVFAKLEQPOEISQRTTIVIOKOTFIAQACVNSTELDELIOQIYVAIINAGIIPGNS 120
Y 121 SNOVSHMDLGSFFPAGTIVTTTIFGNIISPTREGKIFCIIYALLGIPLEFLLAGVGDQ 180
D 121 SNOVSHMDLGSFFPAGTIVTTTIFGNIISPTREGKIFCIIYALLGIPLEFLLAGVGDQ 180
Y 181 LGTFEGKIAKVEDFTFKMNSOTKIRIISTIFILFGCVLFVALPVIKHIKMSALD 240
D 181 LGTFEGKIAKVEDFTFKMNSOTKIRIISTIFILFGCVLFVALPVIKHIKMSALD 240
Y 241 AIYFVITLTITIGFDVYAGSDIEYLDYKPVVFWMLVGLAYFAVLSMIGMLRYIS 300
D 241 AIYFVITLTITIGFDVYAGSDIEYLDYKPVVFWMLVGLAYFAVLSMIGMLRYIS 300
Y 301 KTIKEVGEFFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSVKRLSAGLAGNHNQ 360
D 301 KTIKEVGEFFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSVKRLSAGLAGNHNQ 360
Y 361 ELTPCRRT 368
D 361 ELTPCRMT 368

RESULT 14
PCT-US01-14965-73
Sequence 73, Application PC/TUS0114965
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Roberts, Steven L.
APPLICANT: Benjamin, Christopher
APPLICANT: Karnovsky, Alla M.
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00133.PCT1
CURRENT APPLICATION NUMBER: PCT/US01/14965
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,526
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/216,893
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/223,245
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn version 3.0
SEQ ID NO 73
LENGTH: 543
TYPE: PRT

ORGANISM: Homo sapiens
PCT-US01-14965-73

Query Match 59.9%; Score 1251.5; DB 1; Length 543;
Best Local Similarity 64.3%; Pred. No. 3,4e-110;
Matches 247; Conservative 54; Mismatches 46; Indels 17; Gaps 5;

Y 2 AAPDLLDPKSA-----AONSKPRLSFSSKPPYLASRVSDS--AINMKKKTSTI 50
D 22 AAAYCQPKSKTNPQPPAPATPPRSLSSRAIYVA-K-UTSOGGLQYMKKKTIVAI 80
Y 51 FLVVVYLLIIGAFAKLEQPOEISQRTTIVIOKOTFIAQACVNSTELDELIOQIYVAI 110
D 81 FVVVVVYLVGGLVFALEQPFESSOKNTALEKAEFL-HVGVSPQELTFLIHDAD 140
Y 111 NAGIIPGNSNOVSHMDLGSFFPAGTIVTTTIFGNIISPTREGKIFCIIYALLGIPLE 170
D 141 NAGVSPIGNSSNNSHMDLGSFAFFPAGTIVTTTIFGNIISPTREGKIFCIIYALLGIPLE 200
Y 171 GFLLAGVGDQITFGKIAKVEDFTFKMNSOTKIRIISTIFILFGCVLFVALPVIK 230
D 201 GFLLAGVGDQITFGKIAKVEDFTFKMNSOTKIRIISTIFILFGCVLFVALPVIK 260
Y 231 KHIGWSALDAIYFVITLTITIGFDVYAGG-SDIEYLDYKPVVFWMLVGLAYFAVLS 289
D 261 KYIEGWTALESITFVYVLTITVGFGEFVAGNAGINRENYPLVFWMLVGLAYFAVLS 320
Y 290 SMIGMLRYISKTKKEVGEFFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSV--- 346
D 321 SMIGMLRYISKTKKEVGEFFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSV--- 380
Y 347 -KRLSAGLAGNHNQELTPCRRTL 369
D 381 ERRRLGDQRAHSIDMSPEKRSV 404

RESULT 15
US-09-852-386-73
Sequence 73, Application US/09852386
GENERAL INFORMATION:
APPLICANT: Roberts, Steven L.
APPLICANT: Benjamin, Christopher
APPLICANT: Karnovsky, Alla M.
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00133.US1
CURRENT APPLICATION NUMBER: US/09/852,386
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,526
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/216,893
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/223,245
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn version 3.0
SEQ ID NO 73
LENGTH: 543
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-386-73

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:05:16 ; Search time 24.66 Seconds

(without alignments)
357.486 Million cell updates/sec

Title: US-09-503-089a-2

Sequence: 1 MAAPDLDPKSAQNSKPRL.....LNGLPHCAGEIAVENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 154674 seqs, 21449152 residues

Total number of hits satisfying chosen parameters: 154674

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	5	US-09-336-643-83
2	427	20.3	489	5	US-09-431-367B-2
3	391	18.6	332	5	US-09-431-367B-5
4	363	17.3	394	5	US-09-798-584-15
5	357.5	17.0	365	5	US-09-746-491-60
6	349.5	16.6	374	5	US-09-798-584-1
7	348	16.6	313	5	US-09-431-367B-8
8	348	16.6	313	5	US-09-336-643-81
9	347.5	16.5	330	5	US-09-746-491-59
10	342.5	16.3	258	5	US-09-746-491-61
11	339.5	16.2	330	5	US-09-746-491-58
12	339.5	16.2	333	5	US-09-746-491-22
13	205	9.8	401	5	US-09-431-367B-11
14	153.5	7.3	197	5	US-09-336-643-16
15	150	7.1	205	5	US-09-760-469-1366
16	124.5	5.9	988	6	US-60-299-378-2
17	124.5	5.9	988	6	US-60-299-378-3
18	123	5.9	988	6	US-60-299-378-4
19	123	5.9	988	6	US-60-299-378-5
20	113.5	5.4	221	6	US-60-299-378-21
21	113.5	5.4	221	6	US-60-300-614-21
22	111.5	5.3	962	6	US-60-299-378-4
23	111.5	5.3	962	6	US-60-300-614-4
24	111	5.3	962	6	US-60-299-378-5
25	111	5.3	962	6	US-60-300-614-5
26	111	5.3	989	6	US-60-299-378-6
27	111	5.3	989	6	US-60-300-614-6

28	104	5.0	631	6	US-60-299-484-23	Sequence 23, App1
29	99.5	4.7	254	6	US-60-304-243-6	Sequence 6, App11
30	96	4.6	273	5	US-09-758-472-7	Sequence 7029, Ap
31	95	4.5	613	5	US-09-803-110-1	Sequence 13186, A
32	94	4.5	197	5	US-09-738-626-4	Sequence 4620, Ap
33	94	4.5	355	5	US-09-595-332A	Sequence 1905, Ap
34	93.5	4.5	502	5	US-09-803-110-2	Sequence 12322, A
35	93.5	4.5	1159	6	US-60-299-378-6	Sequence 49, App1
36	93.5	4.5	1159	6	US-60-300-614-4	Sequence 12322, A
37	92	4.4	1209	5	US-09-570-581A	Sequence 785, App
38	91.5	4.4	950	6	US-60-304-243-9	Sequence 9, App1
39	91	4.3	262	5	US-09-760-469-1	Sequence 1371, Ap
40	91	4.3	468	5	US-09-738-626-47	Sequence 4777, Ap
41	91	4.3	468	5	US-09-602-787B-6	Sequence 612, App
42	91	4.3	947	6	US-60-304-243-2	Sequence 2, App11
43	91	4.3	994	6	US-60-304-243-8	Sequence 8, App1
44	91	4.3	1869	5	US-09-573-655A-2	Sequence 1778, Ap
45	91	4.3	1910	5	US-09-573-655A-6	Sequence 681, App

ALIGNMENTS

```

RESULT 1
US-09-336-643-83
; Sequence 83, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutger, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channel
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

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Query Match 99.8% Score 2095; DB Length 411;
Best Local Similarity 99.8%; Pred. No. 3.1e-11; Mismatches 1; Indels 0; Gaps 0;

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1 MAAPDLDPKSAQNSKPRLSFTKPTVLASRVSDTT...KWKVTSTFLVVLVLI 60
11 MAAPDLDPKSAQNSKPRLSFTKPTVLASRVSDTT...KWKVTSTFLVVLVLI 60
61 GATVFKALQPHETISQRTTIVIOKOTFISQHSYNSL...FLIOQYAINAGIIPGNT 120
61 GATVFKALQPHETISQRTTIVIOKOTFISQHSYNSL...FLIOQYAINAGIIPGNT 120
61 GATVFKALQPHETISQRTTIVIOKOTFISQHSYNSL...FLIOQYAINAGIIPGNT 120
121 SNOISHDLSPPFACTVITTTGFGNISPRTEGKIF...VALGIPFLGFLAGVGD 180
121 SNOISHDLSPPFACTVITTTGFGNISPRTEGKIF...VALGIPFLGFLAGVGD 180
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTITFLFC...LEVALPAIIFKHIEGMSALD 240
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTITFLFC...LEVALPAIIFKHIEGMSALD 240
241 AITFVITLTITGIDVAGSDIEYIDFTKPYWPMIL...TANFAVLSMIGMLRVIS 300

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61, 399, 741

Db 241 AIVFVITLITIGFDYVAGSDIEYDFKPVVFWMLVGLAFVAVLSMIGDWLRVIS 300
 QY 301 KKTKEVEGERAAHAEWTANVTAEFKTRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
 Db 301 KKTKEVEGERAAHAEWTANVTAEFKTRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
 QY 361 ELTPCRRRLSVNHLTNERDVLPPLLKTESIYINGLTPHCGEEIAVENIK 411
 Db 361 ELTPCRRRLSVNHLTNERDVLPPLLKTESIYINGLTPHCGEEIAVENIK 411

RESULT 2

US-09-431-367B-2
 ; Sequence 2, Application US/09431367B
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Roy A.J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MNI-074CP
 ; CURRENT APPLICATION NUMBER: US/09/431,367B
 ; CURRENT FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: 09/259,951
 ; PRIOR FILING DATE: 1999-03-01
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 499
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-431-367B-2

Query Match

20.3%; Score 427; DB 5; Length 499;
 Best Local Similarity 31.1%; Pred. No. 2,9e-11;
 Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;

QY 54 VVLYIIGATVFKALDPHEISORTTIVIQKTFISQHSQVNSTELDELIOQIVAAIMAG 113
 Db 12 IIFYLAIGAAIFEVLEBPHEHKEAKKNVYQKHLKEFPCLGEGDLKILEVVSDAAGG 71
 QY 114 IIDLGNSTNSIHWDLGSSFFAGVITTTIGFNGISPRTEGKIFCIYALDIPLEGFL 173
 Db 72 VAITGNQTF--FNMMNPMNAIFATVITTTIGVNAKTPAGHLFCVFGVLPVPL--C 126
 QY 174 LAGVGDLGTIFGKGIKAKVDFEIKMVSOTKIRIISTIFILFGCVLEFALPAIFKHI 233
 Db 127 LHWI-SALGKFFGGRAKRKLQFLTKGVSLSRKQITCTVFIYMGVYLHLVITPPVPMVT 185
 QY 234 EGSWALDAIYVITTTIGFGDYVAG-GSDIEYLDYKFPVFWMLVGLAFVAVLSMT 292
 Db 186 EGMNVIETGLYSPFTTISTIGFQGVAGVNSANYHALRYFVELWITVIGLAW----LSLF 241
 QY 293 GDMLRVTSKTKKEVEGERAAHAEWTANVTAEFKTRRLSVEIYDKFORATSIKRLSA 352
 Db 242 VNM-----KVSSE-----VEVHKAIKRRRR-----RCRESF 267
 QY 353 ELAGNHNOELTPCRRRLSVNHLTNERDV--LPPLKTESIY 391
 Db 268 E-SSPHS-----RKALQVAGSTASKDVNIFLSKKEEY 301

RESULT 3

US-09-431-367B-5
 ; Sequence 5, Application US/09431367B
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Roy A.J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MNI-074CP
 ; CURRENT APPLICATION NUMBER: US/09/431,367B
 ; CURRENT FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: 09/259,951
 ; PRIOR FILING DATE: 1999-03-01
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 5
 ; LENGTH: 332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-431-367B-5

Query Match 18.6%; Score 391; DB 4; Length 332;
 Best Local Similarity 35.9%; Pred. No. 3.2e-11;
 Matches 89; Conservative 51; Mismatches 14; Indels 14; Gaps 6;

QY 50 IFLVVLYIIGATVFKALDPHEISORTTIVIQKTFISQHSQVNSTELDELIOQIVAA 109
 Db 25 LILAYLAVLATGTVGFWTELEGRAADSSRFORDKWEILLFCIDRPALDLSIRDVVOA 84
 QY 110 INAGIIPLGNTSNQIHWDLGSSFFAGVITTTIGFNGISPRTEGKIFCIYALDIPLEGFL 169
 Db 85 YKNGASLSLNTTS-MGRWELVGSFFSVSTTTIGVNLSTMAARLFCIFALVGIPL 143
 QY 170 FGGELLAGVDOLGTIFGKGI---AKVEDTFIKMVSQTKFIIISITIFILFGCVLEVAL 225
 Db 144 NLVVL-----NRLGHLMOQGVNHWASRLGTF--NQ-DPKKALNAGSGLLSGLLFL 195
 QY 226 PAIEFKHIEGWSALDAIYVITTTIGFGDYVAGSDIE-YLDFKPVVFWMLVGLAF 284
 Db 196 PLLFSGHMEGWSYTEGFPYAFITLSTVGFGDYVIGMNPQRRPYLWYKKNVSLMILFGMAW 255
 QY 285 FAVLSMT 292
 Db 256 LALILKLI 263

RESULT 4

US-09-798-584-15
 ; Sequence 15, Application US/09798584
 ; GENERAL INFORMATION:
 ; APPLICANT: Mu, David
 ; APPLICANT: Powers, Scott
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: KCNB: A Novel Potassium Channel Protein
 ; FILE REFERENCE: 016781-00401005
 ; CURRENT APPLICATION NUMBER: US/09/798,584
 ; CURRENT FILING DATE: 2001-03-03
 ; PRIOR APPLICATION NUMBER: US 60/186,951
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 394
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: human potassium channel KIRK3 (TASK1)
 US-09-798-584-15

QY 42 MKWVSTIFLVV--VLYIIGATVFKALDPHEISORTTIVIQKTFISQHSQVNS--T 97
 Db 1 MKRQNVRTALIVCTPTTYLLVGAADFALDSEPELIEROVLRLQOELBARVLSGGYE 60
 QY 98 ELDELIOQIVAAIMAGIIPLGNTSNQIHWDLGSSFFAGVITTTIGFNGISPRTEGK 157
 Db 61 ELERVVLR-LKPKAGV-----QMRPAGSEYFVFTTTIGYHAAPSTDGGRV 108
 QY 158 FCIYALDIPLEGFLLAGDOLGTIF-----GKLVAKVEDTFIKMVSQTKIRI 208
 Db 109 FCMFYALLGIPLTVWFQSTIGERINTLVRLHRAKGI--RRAD-----VSM 156
 QY 209 ISTIIFILFGCVLEVALPAIEFKHIEGWSALDAIYEVVITTTIGFGDYVAGSD--IEY 266

Query Match

17.3%; Score 363; DB 4; Length 394;
 Best Local Similarity 31.0%; Pred. No. 1.5e-11;
 Matches 91; Conservative 59; Mismatches 14; Indels 42; Gaps 9;


```

; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNB (Potassium Channel) expressed in Breast)
US-09-798-584-1

```

```

RESULT 5
US-09-746-491-60
; Sequence 60, Application US/09746491
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; FILE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 365
; SEQ ID NO 60
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-09-746-491-60

```

```

Query Match
Best Local Similarity 17.0%; Score 357.5; DB 5; Length 365;
Matches 94; Conservative 60; Mismatches 109; Indels 49; Gaps 9;

```

```

QY 42 MKKVTSTFLV--VLYLIIGATVEKALDQPHISORTTIVIOKOTFISOHSCVNSTEL 99
DB 1 MKKQNVRTSLIACITFTYLLVGAADFALSDHMEEREKKAKEIRIKKYN--STED 58
QY 100 DELIQIVAA--NAGIIPLGNTSNOISHMDLSSFFPAGVITTTGGFNGISPTREGK 156
DB 59 YRLELVILQSEPHRAGV-----QMKFAGSFYFALITVTTTIGYGHAAFGTDAGK 107
QY 157 IFCTIYALGIPLEFGFLAGVGDLGTFGKGIKAKVEDTPIK-----NVSQTKIR 207
DB 108 AFCEFAVAVLIPILTVMEQSLGERM-----NTEVRALLKRIKCCGMRNTEVS 155
QY 208 IISTIIILFCVLFVALPAIIFKHIEGMSALDAIVFVTLTTIGFDYVAGSD--IE 265
DB 156 MENVVTVGFSCMGCTLCIGAASFQCEBMSFHAHYCCFTITTTIGFDYVALQSKALQ 215
QY 266 YLDFYKPVWFWILVGLVFAVLSMIGDMLRVISKTKKEEVEFRHAA-----EWTA 319
DB 216 RKPFYVAFSFWYILVGLVIGAFILNV--VLRFLTMSDEBERGEGGALPGNPSSVT 273
QY 320 NVTAPEKTRRR 331
DB 274 HISEARQVROR 285

```

```

RESULT 6
US-09-798-584-1
; Sequence 1, Application US/09798584
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A Novel Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; PRIOR FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

```

```

; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNB (Potassium Channel) expressed in Breast)
US-09-798-584-1

```

```

Query Match
Best Local Similarity 16.6%; Score 349.5; DB 5; Length 374;
Matches 106; Conservative 77; Mismatches 116; Indels 63; Gaps 12;

```

```

QY 42 MKKVTSTFLV--VLYLIIGATVEKALDQPHISORTTIVIOKOTFISOHSCVNSTEL 99
DB 1 MKKQNVRTSLIACITFTYLLVGAADFALSDHMEEREKKAKEIRIKKYN--ISSE 59
QY 100 DELIQIVAA--NAGIIPLGNTSNOISHMDLSSFFPAGVITTTGGFNGISPTREGK 157
DB 60 RQLELVILQSEPHRAGV-----QMKFAGSFYFALITVTTTIGYGHAAFGTDAGK 108
QY 158 FCTIYALGIPLEFGFLAGVGDLGTFGKGIKAKVEDTPIK-----NVSQTKIRI 208
DB 109 FCMFYAVLGIPLTVMEQSLGERM-----NTEVRALLKRIKCCGMRNTEVSM 156
QY 209 IISTIIILFCVLFVALPAIIFKHIEGMSALDAIVFVTLTTIGFDYVAGSD--IE 265
DB 157 ENMTVGVGFSCMGCTLCIGAASFQCEBMSFHAHYCCFTITTTIGFDYVALQSKALQ 216
QY 267 YLDFYKPVWFWILVGLVFAVLSMIGDMLRVISKTKR--VGEFRHAA-----EWTA 320
DB 217 KPLVAFSFWYILVGLVIGAFILNV--VLRFLTMSDEBERGEGGALPGNPSSVT 274
QY 321 VTAEFKTRRRRLSVEI-----YDKFORALSKRLSALAGNHNDELPCR 366
DB 275 IPEEPRSRRYKADVDLDQSCCTCYRSDYCGREVA--NPSATLAPHYFHSISKYI 334
QY 367 RTLSVNLHNTNERDYLPLLTSTIYLLGLTPH 398
DB 335 EETSPSTLKN--SLFSPISISPLSHFTDH 364

```

```

RESULT 7
US-09-431-367B-8
; Sequence 8, Application US/09431367B
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNT-074CB
; CURRENT APPLICATION NUMBER: US/09/431,367B
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-8

```

```

Query Match
Best Local Similarity 16.6%; Score 348; DB 5; Length 313;
Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;

```

OY	173	LLAGVGGDLGTFPGKIAKVEDETIKNNVSQTKRIRIISTIIIFLFGCVLVA--LPAIIIF	250
Db	137	LITMSAQSLSL---LTHVPLSLMWKMGMDPRRAACMHLVALLGGVVVFCFLPAVIF	192
OY	231	KHI-EGMSALDAIYEVVLTITFTIGEGDVAGGSDIE-YLDFEYKPVVMFWILYGLATFAAV	288
Db	193	AHLEAWSELDIAFYCFEISTISTIGLDVYGPGEAGQPYRALYKVLVYVFLGLVAVLV	252
OY	289	L 289	
Db	253	L 253	

```

RESULT      8
US-09-336-643-81
US-09-336-643-81
: Sequence 81, Application US/09336643
: GENERAL INFORMATION:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutler, Marc
: APPLICANT: Wang, Jian-Wang
: TITLE OF INVENTION: Novel Human Potassium Channels
: FILE REFERENCE: SEQ-15
: CURRENT APPLICATION NUMBER: US/09/336,643
: CURRENT FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: 60/076,687
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 81
: LENGTH: 313
: TYPE: PRT
: ORGANISM: H. saplens
US-09-336-643-81

```

Query Match	16.6%	Score 348	DB 58	Length 313
Best Local Similarity	34.4%	Pred. No. 2,6e-24		
Matches	83	Conservative	42	Mismatches 104, Indels 12, Gaps 5
QY	57	YLIIGATYFKALQEPHEISQRTTIIYQKOTFISQHSVCNSTELDELLIQIVAINAGIIP	116	
Db	17	YLIYIALLIVARLEGHEARLRALELETFLRAQLLRQSRCSVAAPALDAVERBVLAAAGRGRRV	76	
QY	117	LGNTSNGIS---HMDLGSPFAGVITITIGFNGISPRTEGKICITIIYALIGIPDFG	172	
Db	77	LANAGSNAASDPADPDFAALFFASTILITVVGYYITPLTDAGKASINAFALLGVPTMI	136	
QY	173	LLAGVGDDLTGTFGCGIAKVEDTFIKMNSQTKIRIISTIIPLFSCULFVA--LPAIIF	230	
Db	137	LITTAASQRIISL---LTHVPLSMISMRGMDPRRAACHMLVALLGVVTVCFYLPVAFIF	192	
QY	231	KHI-EGMSALDAIYFVVIYLTITIGFQGVYAGSDIE-YIDFYKPVYWFMLVLAEFAAV	288	
Db	193	AHLEAMSPDLQFYCFIISLTSTIGIGDVIYPGEARPGQPRYALKKVLVYIYLLFGLVAMVLV	252	
QY	289	L 289		
Db	253	L 253		

```

RESULT      9
US-09-746-491--59
: Sequence 59, Application US/09746491
:
: GENERAL INFORMATION:
:   APPLICANT: Burgess, Catherine E.
:   TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
:   FILE REFERENCE: 15966-621

```

```

, CURRENT APPLICATION NUMBER: US/09/746,491
,
, CURRENT FILING DATE: 2000-12-20
,
, PRIOR APPLICATION NUMBER: USSN 60/171,329
,
, PRIOR FILING DATE: 1999-12-21
,
, NUMBER OF SEQ ID NOS: 72
,
, SOFTWARE: PatentIn Ver. 2.0
,
, SEQ ID NO 59
,
, LENGTH: 330
,
, TYPE: PRT
,
, ORGANISM: Homo sapiens
,
, US-09-746-491-59

```

	Query Match	16.5%	Score 347.5	13 %	Length 330;
	Best Local Similarity	34.9%	Pred. No. 3, 1e-24		
	Matches 91; Conservative	42;	Mismatches 95;	Indels 33;	Gaps
Oy	50	IFLVVYLIIIGATVFKALEOPHEISQRTTIVIOKQFISO---	HSCVNSTELDELIQOI	106	
	:	: : : : : :	: : : : : :	:	:
Db	11	LVLCTICLILGAAVFEDALESEAR-SGRORLLNKRGLARRKPFESADYRELERLAQ-		68	
Oy	107	VVAIAGIIPIGNMNSNQSHMDLSSPFEACTVTTITTC:N	SPTREGAKFCETIALLG	166	
	:	: : : : : :	: : : : : :	:	:
Db	69	AEPHRAG-----RQMKRFOSFEFALTVTITIG	"HMACTDSGAKFCPCFYALLG	111	
Oy	167	IPLGEELLGWDOLGITIEGKIARKVEDTF-IKMNVSQFKIT	ISTTIIIFILEGCVEVAL	225	
	:	: : : : : :	: : : : : :	:	:
Db	118	IPLTLVPFQSIGERLINAVVRRLLLAAKCCLOLRMTCVSTE---	NLVVAGLIACCAARTAL	173	
Oy	226	PAIFIKTHIEGSALDAIFYVVITLTITIGFGDVAGSGD	IEYLDFFKPVMW---WIITWL	283	
	:	: : : : : :	: : : : : :	:	:
Db	174	GAVAFSHEGMTEFHAYVYYCITILTITIGDFGVALLQSG	-MLQKKLPYVASPSFLYIITGL	233	
Oy	283	AYFAAIVLSMT-----GDW	295		
	:	: : : : : :	: : : : : :	:	:
Db	233	TVGIAEFLNLVLRPLVASADM	253		

```

RESULT 10
US-09-746-491-61
: Sequence 61: Application US/09746491
: GENERAL INFORMATION:
: APPLICANT: Burgess, Catherine E.
: TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS Encoding Same
: FILE REFERENCE: 15966-621
: CURRENT APPLICATION NUMBER: US/09/746,491
: PRIOR FILING DATE: 2000-12-20
: PRIOR APPLICATION NUMBER: USSN 60/171,329
: PRIOR FILING DATE: 1999-12-21
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 61
: LENGTH: 258
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-746-491-61

```

	Query Match	Similarity	16.3%	Score	342.5	DB 5:	Length	258:	
	Best Local	Similarity	30.0%	Pred.	No. 6.3e-24:				
	Matches	84:	Conservative	61:	Mismatches	94:	Indels	41:	Gaps
Oy	42	MKKRVVSTFLVV--VLVLIIGATFEKALEOEHETISORTVIYIKOTFFISHCVNS--T	97						
		: : :	:	:	: :	:	:	:	:
Dd	1	MKRQNVRLIALIVCFYTLTVGAAFAFDALSEPEMERKRLROIQLRARLNLSGGVE	60						
Oy	98	ELELDLQQIIVAINGGIPLNGTSNQISIMWLGSSFEFAGTVITTGFCNISPREGGKI	157						
		: : : :	:	:	:	: :	:	: :	:
Dd	61	ELERVVLRL-KPKHAGV-----QMRFAGSPFYFAIVITITGYCHAPSTFGSKV	108						
Oy	158	PCIIAALLGIPILFGLLAGVGQDLGTIRCKGIAKVEDTIANNVSOTK-----IN	208						
		: :	:	:	:	: :	:	: :	:
Dd	109	FCMFALLGIPILTVAFPOSIGERI-----NTEVRILLRRAKKGLGMRAAEVSM	156						

Oy	54	VVLIIIGATVFKALDEQHEHLSQRTTIVIOKOTFISQHS,VNSUEDELLOQIYAAINAG	113
Dd	47	LVTALVAALVFSALE-----DQOVLVA-----DOEFKEELICRIIMCS	89
Oy	114	IIPLGNTS-----NOISHMDGSSFFFAV-----WTFEGNISPRETEGGIF	158
Dd	90	ETVEDRKRQDLOGHLQAKKKPQMFRNTHMSTLSSLFCOCTSTVGXGYIYPTVRLKYL	149
Oy	159	CITIALGLPIPLFGLLLAGVDOLGT-----FGKGIANVDTFTKM-----	199
Dd	150	CMLYALEGIPLMFLVLDTDGDIALTILSTSYNRRKKPPFTRPLLKWCPSKSLFKKKRPD	209
Oy	200	-----	199
Dd	210	KPADEAVPOIIISAELPGPKLTGCPSPSCSMELFEHSIALEKONTLOLPQAMERSNS	266
Oy	200	-----NWSQT-----KRIISTITFIPLHGCVLFVALPAITEKHIEG	235

Db 270 CPELVGRLSYISINDEVGQOVERLDIPPLIALIVFAISCAAMI-LPF----- 320
QY 236 W-SALD---AIYFVITLTITIGD-----YVAGSDIEY-----L 267
Db 321 WETQLEENAFYFCFVLTITIGFDVLEHPNPFLEFSPSIYIYGMETVFAFKLVQRLI 380
QY 268 DFKPVVWF 277
Db 381 DIKNWMLFF 390

RESULT 14

US-09-336-643-16
; Sequence 16, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rulter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 197
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-16

Query Match 7.38; Score 153.5; DB 5; Length 197;
Best Local Similarity 27.58; Pred. No. 9e-07;
Matches 52; Conservative 39; Mismatches 65; Indels 33; Gaps 8;

QY 148 ISPTREGKIFCIYIALGIPFLAGVDDIGTFGKIAKVEDTFIKWNVSQTKIR 207
Db 1 MAPLSGGRKFCVAVYALGIPASIALVATIRHCLLPVLSRPAAVY---VHQLSPARAA 57
QY 208 IISTIFILEFCVLPALPAIFKHIEG-WSALDAIYFVVITLTIGFDYVAG-GSDIE 265
Db 58 LLOAVNALGLVASSFVLLPALVLMGQDCLGAVYFCFSSISTIGLEDLLPGRGRSLH 117
QY 266 YLDFYKPVWF-----WILGLAVFAFVLSMIGDMLRVISKTKKEEYGEFRAHAEN 317
Db 118 -----PVYIHGQALLGLVLLGL-----LAML-----LAVETSELPOVRAMGKFF 159
QY 318 --TANYTAE 324
Db 160 RPSGPVTAE 168

RESULT 15

US-09-760-469-1386
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1386
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1386

Query Match 7.18; Score 150; DB 5; Length 205;
Best Local Similarity 30.28; Pred. No. 2e-07;
Matches 39; Conservative 28; Mismatches 50; Indels 12; Gaps 6;

QY 197 IKWVNSQTKIRIISTII--FILFGCVLFVALPAIFKH1--GWSALDAIYFVVITLTIG 253
Db 39 IRMGFSKQVVAIYHAYVLGFTVVSCEFFI--PAAVFSV1--NPLESFYFCISISTIG 96
QY 254 FGDYVAG-GSDIEYLDYKPVVWFMLVGLAYFAAVLSMIGDLRVYSK-----KTKEEV 307
Db 97 LGDYVPGEGYNOKFRELYKIGTICVLLGLIAMLVLEFCE-LHELIKFRKMKFYVKKDK 155
QY 308 GEFRRAHAE 316
Db 156 DEDQVHIE 164

Search completed: August 28, 2001, 17:11:44
Job time: 388 sec

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[illegible]

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RESULT      2
US-09-431-367B-2
: Sequence 2, Application US/09431367B
:
: GENERAL INFORMATION:
:
: APPLICANT: CUTLIS, RORY A.J
:
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
:
: FILE REFERENCE: NMI-074CP
:
: CURRENT APPLICATION NUMBER: US/09/431,367B
:
: CURRENT FILING DATE: 1999-11-01
:
: PRIOR APPLICATION NUMBER: 09/259,951
:
: PRIOR FILING DATE: 1999-03-01
:
: NUMBER OF SEQ ID NOS: 12
:
: SOFTWARE: patentln Ver. 2.0
:
: SEQ ID NO 2
:
: LENGTH: 499
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-09-431-367B-2

```

Query Match	20.1%;	Score 420;	DB 5;	Length 499;
Best Local Similarity	30.8%;	Pred. No. 4.5e-31;		
Matches 105;	Conservative 62;	Mismatches 120;	Indels 54;	Gaps 11

[illegible]

```

RESULT      3
US-09-431-367B-5
; Sequence 5, Application US/09431367B
; GENERAL INFORMATION:
; APPLICANT: Curtis, RORY A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-5

```

Query Match	18.5%	Score 387;	DB Length 332;
Best Local Similarity	35.5%;	Pred. No. 2.9e-27;	
Matches 88;	Conservative 51;	Mismatches 5;	Indels 14; Gaps 6;

0Y 50 IFVVVYVYLLIIIGAANFRALEPOBISQRTITVIOKOFIFA .CVNTEDELITQOYVA 109
 0Y 25 LILAYLAVLALGTGVFTLEBRAADSSRQOROKWELLFh:1:1:UDPALDSILIRVOYA 84
 0Y 110 INAGIIPUGNSSNOVSHWDIGSSFFGAVYVTTIGFEN1 .FEGKIFCIYALGLIP 169
 Db 85 YKNGASILSTNFTS -MGREIIVGSEFFSVSTTIGYCNLSINMAHLCIFPALVGIP 143
 0Y 170 FGEILLAGVDGLTFEGGI----AKVEDPFIRKNNVSOTR14:1STI1F1IFPGCVFVAL 225
 Db 144 NLVYL----NRLGHIMOGGVNMMASRLIGT--WQ-DPDKr:LAUSGALLSGLLEPLL 195
 0Y 226 PAVIFKIHIEGMSALDAIFVVYVTTTIGCGDYVAGSGDIE:1:DPYKPVVFWILVGLAY 284
 Db 196 PPLLEFSHMEGNSYTEGEFFAFITILSTYGVGDIYVIGMNPSCRYPLMY:ANNNSWILTEGMAN 255
 0Y 285 FAAYLSMT 292
 Db 256 LALIIKLI 263

RESULT 4
US-09-798-584-15

```

US-09-798-584-15
Sequence 15, Application US/09798584
GENERAL INFORMATION:
APPLICANT: Mu, David
APPLICANT: Powers, Scott
APPLICANT: Tuttle, Inc.
TITLE OF INVENTION: KCNBJ: A Novel Potassium Channel Protein
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09-798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human potassium channel KCNBJ (TASK1)
US-09-798-584-15

```

Query Match	17.7%;	Score 370;	DB E	Length 394;
Best Local Similarity	28.0%;	Pred. No. 1.4e+6;		
Matches 109;	Conservative 66;	Mismatches 145;	Indels 88;	Gaps 13

```

QY 42 MAMKVYITFLVY--VLKLIIGAANFKALBPQELSORK VIOKJCFILAGHACVNS--T 97
Db 1 MKRQWVRLLALICFTYLLLVGLGAAVLESEPELIEKCP ELQPOELRARIY NLQGYE 60
QY 98 ELDELIIQIVAINNGIILPLGNSSNQVSHMDLSSFFRA LPTITIGGNISPTBEGKI 157
Db 61 ELERVLRL-KPKHGV-----QMPFAGSEFFA LPTITIGYGAAPSTDGKV 108
QY 158 FCIIVALLGIPFLGAGVGDGLGITF-----GRKLVKVEDPFIKVNVSOTKIRI 208
Db 109 FMPFALIGIPFLTLMFQSLSEBRINTLRYLLHRAKGL LKAD-----VSM 156
QY 209 ISTIIFILFGCVLFAVLEAVIFKHIEGMSALDAIFYVITL TIGFDYVAGGSD-TEY 266

```


[illegible]

```

RESULT 5
US-09-746-491-59
: Sequence 59, Application US/09746491
: GENERAL INFORMATION:
: APPLICANT: Burgess, Catherine E.
: TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 15966-621
: CURRENT APPLICATION NUMBER: US/09/746,491
: CURRENT FILING DATE: 2000-12-20
: PRIOR APPLICATION NUMBER: USSN 60/171,329
: PRIOR FILING DATE: 1999-12-21
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 59
: LENGTH: 330
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-746-491-59

```

Query Match	16.8%	Score 351.5	DB 5	Length 330
Best Local Similarity	35.0%	Pred. No. 5.7e-25		
Matches 91; Conservative 44; Mismatches 94;				Indels 31; Gaps 8

[illegible]

```

RESULT      6      US-09-746-491-60
Sequence 60 Application US/09746491
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIORITY APPLICATION NUMBER: USSN 60/171,329
PRIORITY FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72

```

```

; SOFTWARE:PatentIn Ver. 2.0
; SEQ ID NO: 60
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-09-746-491-60

```

Query Match	16.8%;	Score 351.5;	Length 365;
Best Local Similarity	30.1%;	Pred. No. 6.6e-47;	
Matches	94;	Conservative	59;
		Mismatches	17;
		Indels	49;
		Gaps	9

Qy	42	MKMTVSTIFLVV--VLYLIIIGAAVFALNEPOEISQFTVIGQRFPIIOMHCAVNSTEL	99
Db	1	MKKQVVRSLSLIACFTFYLLVGAAVFALDESDEHRELLKAEIRIRQKYNL--STED	58
Qy	100	DELIIQIYAAL---NAGIIFPLGNSSNOVSHMDLSSFTFAGVTTIGFGNISPRIDEGK	156
Db	59	YRQLETVLLOSEPFRAGV-----QKRFAGSYEFALITTTTGYGHAAPGIDAGK	107
Qy	157	IFCLIIYALIGIPLEGFLAGVGDOLGTIFGKGIKVEDIEFLAN-----NVSQTKIR	207
Db	108	AFCEMFYAVLGIPLPLVMHQSLGEMR-----NLHFVLELRKIRKCCGMRNTEVS	155
Qy	208	IISTIFILFECVLEFVALPANIIFKHIQESMLDIITFVITHTITIGGDIYVAGSD--IE	265
Db	156	MENNAVTVGFECQKGTLCIGAAAFSQCEBSEFHAHYVCFHTTIGGDIYVALOSKALQ	215
Qy	266	YLDEFKPPVVMIIIVGLAYFAAVLSMIGDMIRVYSKRTLTFEFRHAA-----EMTA	319
Db	216	RKPFVFAVSFMIIIVGLVIGLAFNLNV--VLRFLTMNS-----EGEGCALPQNPSSVYT	273
Qy	320	NVTAIEFKETRRR	331
Db	274	HISEEARQVRR	285

```

RESULT 7
Sequence 61, Application US/09746491-61
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ. ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 258
TYPE: PRT
ORGANISM: Mus musculus
US-09-746-491-61

```

Query Match	16.88;	Score 350.5;	Length 258;
Best Local Similarity	31.22;	Prod. No. 5e-25;	
Matches 88;	Conservative 60;	Mismatches 89;	Indels 45; Gaps

Oy	42	KKWKVSTPLFV--VLTLIGAAGFKALEOPQEIISQRTIV QKQTFIAOHACVNSTEL	99
		: : : : : : : : : : : : : : : : : : : : : : : :	
Db	1	MKRQVRFALIVCFYFLLVGAAGFALDSEPMIEKGRFLQLELRAR---NLSEG	57
Oy	100	D-ELIQIVAAI---NAGIPLGNSSNOVSHWDLGSSFFERV VITITGQNISPRTEG	155
		: : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	58	GYEELERVVLRLKPHKAGV-----OMRFGSGSYVAIVITITGIGHAPSDSG	106
Oy	156	KIFCIYVALLGPIPLGFLLAGVGQDGLGTFCKGLAKVEL PTKNNVSOTK-----I	206
		: : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	107	KVPCFVALLGPIPLLVFQSLGRT-----NII VRLRLHPRKGLGCMRAEV	154

Db 157 ENNVATGPFSCMGTLGIGAAAFSCOEEMSEFHAYVCFITLTTIGFDYVALQTKALQK 216
QY 267 LDFKPVWEMILVGLAYFAAFLSMIGDMLRVISKTKREE--VGEFRAHAA---EWTAN 320
Db 217 KPLVARSFMVILVGLVIGAFILNV--VLEFLMNSDEDERADREERASLAGNNNSVYIH 274
QY 321 VTAEKETRRRLSVEI-----YDKFORATSVKRLISAELAGNHNDELTPCR 366
Db 275 IPEBRRSRPRYKADVPDLQSVCSCTCYRSODYGCRSVAPDQNSFSAKLAPHYFHSIS--Y 332
QY 367 RTLSVNLHLSEREVLPPRLAKESIYINGLTPH 398
Db 333 KIEIISPTLKNLSFPSPISISIPGLHSFTDH 364

RESULT 11
US-09-431-367B-8
Sequence 8, Application US/09431367B
GENERAL INFORMATION:
APPLICANT: Curtiss, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-431-367B-8

Query Match 16.4%; Score 342; DB 5; Length 313;
Best Local Similarity 34.4%; Pred. No. 4e-24;
Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;

QY 57 YLIIGAANFKALBQPOEISQRTTIVIOKQFIQAQACVNSTEDELLOQIYAIAINAGIIP 116
Db 17 YLVGALLVARLBEGPHARLRAELETLRADLQRSPCVAAPALDAFVERVLAAGRLGRV 76
QY 117 LGNSSNOVS---HMDIGSFFAGVITTTIGFNGISPRTEGKIFCIYALGIPLEGF 172
Db 77 LANSSGANSNDPAMDASALFFASTLTITVGYCTTLPDAGAFSAIARLLGVPPTML 136
QY 173 LLAGVGDLGTIFGKGIKAKVEDFTIKMNSQTKIRIISITIFILEGCVLFA--LPVAVIF 230
Db 137 LTFASAGRLSL---LTHVPLSWLSMRMGMDPRRACMHLVALLGVVTVCFVPAVIF 192
QY 231 KHI-EGMSALDAIFYVITTTIGFGDYVAGGSDIE-YLDFKRVWFMILVGLAYFAAV 288
Db 193 AHLEEANSFLDAFYCFISLSTIGLDYVPEAGOPPRALRYLVTVYVLEFLGIVAMLV 252
QY 289 L 289
Db 253 L 253

RESULT 12
US-09-336-643-81
Sequence 81, Application US/09336643
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 81
LENGTH: 313
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643-81

Query Match 16.4%; Score 342; DB 5; Length 313;
Best Local Similarity 34.4%; Pred. No. 4e-24;
Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;

QY 57 YLIIGAANFKALBQPOEISQRTTIVIOKQFIQAQACVNSTEDELLOQIYAIAINAGIIP 116
Db 17 YLVGALLVARLBEGPHARLRAELETLRADLQRSPCVAAPALDAFVERVLAAGRLGRV 76
QY 117 LGNSSNOVS---HMDIGSFFAGVITTTIGFNGISPRTEGKIFCIYALGIPLEGF 172
Db 77 LANSSGANSNDPAMDASALFFASTLTITVGYCTTLPDAGAFSAIARLLGVPPTML 136
QY 173 LLAGVGDLGTIFGKGIKAKVEDFTIKMNSQTKIRIISITIFILEGCVLFA--LPVAVIF 230
Db 137 LTFASAGRLSL---LTHVPLSWLSMRMGMDPRRACMHLVALLGVVTVCFVPAVIF 192
QY 231 KHI-EGMSALDAIFYVITTTIGFGDYVAGGSDIE-YLDFKRVWFMILVGLAYFAAV 288
Db 193 AHLEEANSFLDAFYCFISLSTIGLDYVPEAGOPPRALRYLVTVYVLEFLGIVAMLV 252
QY 289 L 289
Db 253 L 253

RESULT 13
US-09-431-367B-11
Sequence 11, Application US/09431367B
GENERAL INFORMATION:
APPLICANT: Curtiss, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-09-431-367B-11

Query Match 10.1%; Score 212; DB 5; Length 401;
Best Local Similarity 20.8%; Pred. No. 6.7e-11;
Matches 77; Conservative 37; Mismatches 104; Indels 172; Gaps 11;

QY 54 VLVLIIGAANFKALBQPOEISQRTTIVIOKQFIQAQACVNSTEDELLOQIYAIAINAG 113
Db 47 LVYALVGAIVFSAIEDGOVL-----VDFEFKFLLELCRIINCS 89
QY 114 IIPGNS-----NOVSHMDIGSFFAGVITTTIGFNGISPRTEGKIF 158
Db 90 ETVEEDKRODLQGLQVKKPQWPKRTHMSFLSFLFCCTG-STVGYIYIPVTRLGKYL 149
QY 159 CIIVALLGIPILFGLLAGVGDLGTI-----FGKGI-----FFINW----- 199

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Db 150 CMLYALFGLPMFLVLTGDDIATLSTSYNRFKPFPTRLSLKWCPSLKKKPPD 209
QY 200 ----- 199
Db 210 KPADEAVPQIIISAEELPGKLTCTSPSCSMELEFERSHALEKONTLQLPQAMERSNS 269
QY 200 -----NVSQT-----KIRIISTIIIFGCVLFVALPAVIFKHIEG 235
Db 270 CPELVGLRLSYIISNMLEVGOOVERLDIPLPIIALIVFAVISCANAAL-LPF----- 320
QY 236 W-SALD---AIYFVITLTITIGRD-----YVAGSDEY-----L 267
Db 321 WETQULPENAFYFCFVLTITIGFDVLEHPNPFLEFSIYIIVGMETVFAELVONRLI 380
QY 268 DFYKPVVWF 277
Db 381 DIKNWMLPF 390

```

```

RESULT 14
US-09-336-643-16
; Sequence 16, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FASTED for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 197
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-16

```

```

Query Match 7.3%; Score 152.5; DB 5; Length 197;
Best Local Similarity 27.5%; Pred. No. 8.1e-07;
Matches 52; Conservative 39; Mismatches 65; Indels 33; Gaps 8;

```

```

QY 148 ISPRTEGKIFCTIVALLGIFLPGVLDGDLGTFIIGKIAKVEDTFIKWVSOTKIR 207
Db 1 MAPLSPGGAFCFVYALGIPASLALVATLRHCLLPVLSRPAWVA---VHWQLSPARA 57
QY 208 IISTIIIFGCVLFVALPAVIFKHIEG--WSALDAIYFVITLTITIGFGDYVAG--GSDIE 265
Db 58 LQGVAVLGLLVASFFVLPLPALVLMGLGDCSILGAVYFCSSLSLTIGLEDLPGRGSLH 117
QY 266 YLDFYRPVWF-----WILVGLAYFAVLSMIGDMLRVISKTKREYGEFFRAHAEM 317
Db 118 -----PVIYHLGQLALLGLYLLGL-----LAML-----LAVTFSELQVRAWGKFF 159
QY 318 --TANYTAE 324
Db 160 RPSGPVTAE 168

```

```

RESULT 15
US-09-760-469-1386
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:

```

```

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1386
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1386

```

```

Query Match 7.2%; Score 151; DB 5; Length 205;
Best Local Similarity 30.2%; Pred. No. 1.2e-07;
Matches 39; Conservative 28; Mismatches 11; Indels 12; Gaps 6;

```

```

QY 197 IKWVSQTKIRIISTII--FILEGCVLFVALPAVIFKH--WSALDAIYFVITLTITIG 253
Db 39 IRMGFSKQVVAIVHVLGFTVYSCFFI--PAVRSVL DNMFLFSYFCFISLSTIG 96
QY 254 FGDYVAG--GSDIEYLDYFYPVWFILVGLAYFAVLSKIGMLRVISK-----KTKREV 307
Db 97 LGDYVAGEGYNOKFRRLYKIGITCYLLGLIAMLVLET CE-LHELKKFRKMFYVKKDK 155
QY 308 GEFRAHAE 316
Db 156 DEDQVHIIE 164

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Search completed: August 28, 2001, 17:11:45
Job time: 389 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:01:11 ; Search time 242.67 Seconds
(without alignments)
375.734 Million-cell updates/sec

Title: US-09-503-089A-2

Perfect score: 2100
Sequence: 1 MAAPDLDPKSAQNSKPRL.....LNGLPHCAGEEIAVENIK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2803329 segs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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2: /cgn2_6/ptodata/2/paa/US06.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2100	100.0	411	19 US-09-503-089A-2	Sequence 2, Appl
2	2095	99.8	411	1 PCT-US99-03826-83	Sequence 83, Appl
3	2095	99.8	411	17 US-09-336-643-83	Sequence 83, Appl
4	2095	99.8	411	17 US-09-336-643-83	Sequence 83, Appl
5	2095	99.8	411	22 US-09-828-746-2	Sequence 2, Appl
6	2062	98.2	426	12 US-08-816-011-45	Sequence 45, Appl
7	2062	98.2	426	12 US-08-816-011A-45	Sequence 45, Appl
8	2062	98.2	426	12 US-08-816-011C-45	Sequence 45, Appl
9	2041	97.2	411	19 US-09-503-089A-4	Sequence 4, Appl
10	2035	96.9	411	22 US-09-828-746-6	Sequence 6, Appl

11	1833	87.3	370	20 US-09-655-272-4	Sequence 4, Appl
12	1824	86.9	370	15 US-09-144-914-8	Sequence 8, Appl
13	1824	86.9	370	18 US-09-436-265-8	Sequence 8, Appl
14	1243	59.2	543	1 PCT-US01-14965-73	Sequence 73, Appl
15	1243	59.2	543	22 US-09-852-386-73	Sequence 73, Appl
16	1241.5	59.1	657	23 US-60-207-583-37	Sequence 376, Appl
17	1215.5	57.9	724	23 US-60-216-547-10	Sequence 10, Appl
18	1205	57.4	484	23 US-60-230-445-17	Sequence 1632, Ap
19	803	38.2	392	1 PCT-US00-349838	Sequence 55, Appl
20	803	38.2	392	21 US-09-729-739-7	Sequence 55, Appl
21	803	38.2	393	18 US-09-432-470-7	Sequence 2, Appl
22	803	38.2	393	18 US-09-432-470-6	Sequence 2, Appl
23	803	38.2	419	22 US-09-828-035-3	Sequence 2, Appl
24	803	38.2	440	23 US-60-258-275-5	Sequence 424, App
25	803	38.2	1314	1 PCT-US00-349838	Sequence 29, Appl
26	803	38.2	1314	21 US-09-729-739-7	Sequence 29, Appl
27	776.5	37.0	398	20 US-09-655-272-4	Sequence 2, Appl
28	759.5	36.2	1779	23 US-60-212-358-1	Sequence 133, Appl
29	759.5	36.2	1785	23 US-60-207-416-9	Sequence 91, Appl
30	758	36.1	1616	23 US-60-229-525-3-1	Sequence 331, App
31	638.5	30.4	1068	23 US-60-212-358-1-5	Sequence 195, Appl
32	547	26.0	107	22 US-09-828-746-6	Sequence 4, Appl
33	519	24.7	110	23 US-60-171-487-5	Sequence 594, App
34	513	24.4	295	23 US-60-223-269-8	Sequence 8, Appl
35	427	20.3	499	16 US-09-259-951-2	Sequence 2, Appl
36	427	20.3	499	16 US-09-259-951-2	Sequence 4, Appl
37	427	20.3	499	17 US-09-357-425-6	Sequence 6, Appl
38	427	20.3	499	18 US-09-436-265-7	Sequence 28, Appl
39	427	20.3	499	19 US-09-561-763-7	Sequence 2, Appl
40	427	20.3	499	21 US-09-735-169-4	Sequence 2, Appl
41	427	20.3	499	21 US-09-735-169-4	Sequence 4, Appl
42	427	20.3	499	21 US-09-735-169A-7	Sequence 2, Appl
43	427	20.3	499	21 US-09-735-171-2	Sequence 2, Appl
44	427	20.3	499	21 US-09-735-171-4	Sequence 4, Appl
45	427	20.3	499	21 US-09-735-171A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-503-089A-2
Sequence 2, Application US/09503089A
GENERAL INFORMATION:
APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: LESAGE, FLORIAN
APPLICANT: ROMER, GEORGES
APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identification of anesthetics
FILE REFERENCE: f1b12prov3-humanantrex
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-09-503-089A-2

Query Match	100.0%	Score 2100;	E 19;	Length 411;
Best local Similarity	100.0%	Pred. No. 1.6;	03;	Indels 0;
Matches 411;	Conservative 0;	Mismatches 0;	Gaps 0;	
QY	1	MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTT1	AKKTVSTTFLVVLVYLII 60	
DB	1	MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTT1	AKKTVSTTFLVVLVYLII 60	
QY	61	GATVFAALQPHRISORTIVIVOKOFIFISHGCVNSTEL	ILLOQIVAAINAGIIPLGNT 120	
DB	61	GATVFAALQPHRISORTIVIVOKOFIFISHGCVNSTEL	ILLOQIVAAINAGIIPLGNT 120	

```

OY 121 SNOISHMDLGSSFFAGVITTTIGFNGISPRTEGKIFCIITIALGIPLEFGLAGVGO 180
    |||||||
Db 121 SNOISHMDLGSSFFAGVITTTIGFNGISPRTEGKIFCIITIALGIPLEFGLAGVGO 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSOTKIRIITIIIFILPGCVLPAALPIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAKVEDPFIKNNVSOTKIRIITIIIFILPGCVLPAALPIFKHIEGMSALD 240
OY 241 AIYFVITTTTIGFGDYVAGSDIEYLDYKPYVWFMIIWGLAYFAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AIYFVITTTTIGFGDYVAGSDIEYLDYKPYVWFMIIWGLAYFAAVLSMIGDMLRVIS 300
OY 301 KKTKEEVGEFRAHAAMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCRRITLSVNHILTNERDVLPLPKTESIYLANGLTPHCAGEIYAVIENIK 411
    |||||||
Db 361 ELTPCRRITLSVNHILTNERDVLPLPKTESIYLANGLTPHCAGEIYAVIENIK 411

```

RESULT 2

```

PCT-US99-03826-83
; Sequence 83, Application PC/TUS9903826A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEO-15PCT
; CURRENT APPLICATION NUMBER: PCT/US99/03826A
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
PCT-US99-03826-83

```

Query Match 99.8%; Score 2095; DB 1; Length 411;

Best Local Similarity 99.8%; Pred. No. 5.2e-203;

Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMMKWTSTFLVVLXLI 60
    |||||||
Db 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMMKWTSTFLVVLXLI 60
OY 61 GATVFALKEPHEISORTITIVIOKOTFISQHSVCNSTEDELIIQOIVAAINAGIIPLGNT 120
    |||||||
Db 61 GATVFALKEPHEISORTITIVIOKOTFISQHSVCNSTEDELIIQOIVAAINAGIIPLGNT 120
OY 121 SNOISHMDLGSSFFAGVITTTIGFNGISPRTEGKIFCIITIALGIPLEFGLAGVGO 180
    |||||||
Db 121 SNOISHMDLGSSFFAGVITTTIGFNGISPRTEGKIFCIITIALGIPLEFGLAGVGO 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSOTKIRIITIIIFILPGCVLPAALPIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAKVEDPFIKNNVSOTKIRIITIIIFILPGCVLPAALPIFKHIEGMSALD 240
OY 241 AIYFVITTTTIGFGDYVAGSDIEYLDYKPYVWFMIIWGLAYFAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AIYFVITTTTIGFGDYVAGSDIEYLDYKPYVWFMIIWGLAYFAAVLSMIGDMLRVIS 300
OY 301 KKTKEEVGEFRAHAAMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
    |||||||

```

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Db 301 KKTKEEVGEFRAHAAMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCRRITLSVNHILTNERDVLPLPKTESIYLANGLTPHCAGEIYAVIENIK 411
    |||||||
Db 361 ELTPCRRITLSVNHILTNERDVLPLPKTESIYLANGLTPHCAGEIYAVIENIK 411

```

RESULT 3

```

US-09-336-643-83
; Sequence 83, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; APPLICANT: Ping Hu
; APPLICANT: Marc Rutter
; APPLICANT: Jian-Ying Wang
; TITLE OF INVENTION: Novel Human Potassium Cha
; FILE REFERENCE: SEO-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; EARLIER FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: PCT/US99/03826
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

```

Query Match 99.8%; Score 2095; DB 1; Length 411;

Best Local Similarity 99.8%; Pred. No. 5.2e-203;

Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMMKWTSTFLVVLXLI 60
    |||||||
Db 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMMKWTSTFLVVLXLI 60
OY 61 GATVFALKEPHEISORTITIVIOKOTFISQHSVCNSTEDELIIQOIVAAINAGIIPLGNT 120
    |||||||
Db 61 GATVFALKEPHEISORTITIVIOKOTFISQHSVCNSTEDELIIQOIVAAINAGIIPLGNT 120
OY 121 SNOISHMDLGSSFFAGVITTTIGFNGISPRTEGKIFCIITIALGIPLEFGLAGVGO 180
    |||||||
Db 121 SNOISHMDLGSSFFAGVITTTIGFNGISPRTEGKIFCIITIALGIPLEFGLAGVGO 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSOTKIRIITIIIFILPGCVLPAALPIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAKVEDPFIKNNVSOTKIRIITIIIFILPGCVLPAALPIFKHIEGMSALD 240
OY 241 AIYFVITTTTIGFGDYVAGSDIEYLDYKPYVWFMIIWGLAYFAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AIYFVITTTTIGFGDYVAGSDIEYLDYKPYVWFMIIWGLAYFAAVLSMIGDMLRVIS 300
OY 301 KKTKEEVGEFRAHAAMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCRRITLSVNHILTNERDVLPLPKTESIYLANGLTPHCAGEIYAVIENIK 411
    |||||||
Db 361 ELTPCRRITLSVNHILTNERDVLPLPKTESIYLANGLTPHCAGEIYAVIENIK 411

```

RESULT 4

```

US-09-336-643-83
; Sequence 83, Application US/09336643A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.

```


APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
EARLIER APPLICATION NUMBER: 60/076,687
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 411
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643-83

Query Match 99.8%; Score 2095; DB 17; Length 411;
Best Local Similarity 99.8%; Pred. No. 5.2e-203;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MAADLLDPKSAONSKPRLSFTKPTVLASRVSDTTINVMKKKTVSTIFLVVLYLI 60
1 MAADLLDPKSAONSKPRLSFTKPTVLASRVSDTTINVMKKKTVSTIFLVVLYLI 60
61 GATVFKALEOPHEISORTTIVIOKOTFISQHCNSTEELDIOOYVAIINAGIIPLGNT 120
61 GATVFKALEOPHEISORTTIVIOKOTFISQHCNSTEELDIOOYVAIINAGIIPLGNT 120
61 GATVFKALEOPHEISORTTIVIOKOTFISQHCNSTEELDIOOYVAIINAGIIPLGNT 120
121 SNOISHMDLSSFFAGTIVITIGFGNISPTREGKIFCIYALGIPFGLAGVDQ 180
121 SNOISHMDLSSFFAGTIVITIGFGNISPTREGKIFCIYALGIPFGLAGVDQ 180
121 SNOISHMDLSSFFAGTIVITIGFGNISPTREGKIFCIYALGIPFGLAGVDQ 180
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVFVALPAIIFKHIGWSALD 240
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVFVALPAIIFKHIGWSALD 240
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVFVALPAIIFKHIGWSALD 240
241 AIYFVITLTITIGFDYVAGSDIEYLDYKPVVFWMLVGLAFVAVLSMIGMLRYIS 300
241 AIYFVITLTITIGFDYVAGSDIEYLDYKPVVFWMLVGLAFVAVLSMIGMLRYIS 300
241 AIYFVITLTITIGFDYVAGSDIEYLDYKPVVFWMLVGLAFVAVLSMIGMLRYIS 300
301 KKTKEEVEGFRAHAEMTANTAFKETRRLSVEIYDKFQRAISIKRKLASAEIAGNHQ 360
301 KKTKEEVEGFRAHAEMTANTAFKETRRLSVEIYDKFQRAISIKRKLASAEIAGNHQ 360
301 KKTKEEVEGFRAHAEMTANTAFKETRRLSVEIYDKFQRAISIKRKLASAEIAGNHQ 360
361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411
361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411
361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411

RESULT 5
US-09-828-746-2
Sequence 2, Application US/09828746
GENERAL INFORMATION:
APPLICANT: Helen Jane Meadows
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30031-D1
CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/236,080
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: EP 98300570.3
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: UK 9822135.1
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 6

26020025485

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-828-746-2

Query Match 99.8%; Score 2095; DB 42; Length 411;
Best Local Similarity 99.8%; Pred. No. 5.2e-43;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MAADLLDPKSAONSKPRLSFTKPTVLASRVSDTTINVMKKKTVSTIFLVVLYLI 60
1 MAADLLDPKSAONSKPRLSFTKPTVLASRVSDTTINVMKKKTVSTIFLVVLYLI 60
61 GATVFKALEOPHEISORTTIVIOKOTFISQHCNSTEELDIOOYVAIINAGIIPLGNT 120
61 GATVFKALEOPHEISORTTIVIOKOTFISQHCNSTEELDIOOYVAIINAGIIPLGNT 120
61 GATVFKALEOPHEISORTTIVIOKOTFISQHCNSTEELDIOOYVAIINAGIIPLGNT 120
121 SNOISHMDLSSFFAGTIVITIGFGNISPTREGKIFCIYALGIPFGLAGVDQ 180
121 SNOISHMDLSSFFAGTIVITIGFGNISPTREGKIFCIYALGIPFGLAGVDQ 180
121 SNOISHMDLSSFFAGTIVITIGFGNISPTREGKIFCIYALGIPFGLAGVDQ 180
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVFVALPAIIFKHIGWSALD 240
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVFVALPAIIFKHIGWSALD 240
181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVFVALPAIIFKHIGWSALD 240
241 AIYFVITLTITIGFDYVAGSDIEYLDYKPVVFWMLVGLAFVAVLSMIGMLRYIS 300
241 AIYFVITLTITIGFDYVAGSDIEYLDYKPVVFWMLVGLAFVAVLSMIGMLRYIS 300
241 AIYFVITLTITIGFDYVAGSDIEYLDYKPVVFWMLVGLAFVAVLSMIGMLRYIS 300
301 KKTKEEVEGFRAHAEMTANTAFKETRRLSVEIYDKFQRAISIKRKLASAEIAGNHQ 360
301 KKTKEEVEGFRAHAEMTANTAFKETRRLSVEIYDKFQRAISIKRKLASAEIAGNHQ 360
301 KKTKEEVEGFRAHAEMTANTAFKETRRLSVEIYDKFQRAISIKRKLASAEIAGNHQ 360
361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411
361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411
361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411

RESULT 6
US-08-816-011-45
Sequence 45, Application US/08816011
GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
TITLE OF INVENTION: Encoding Them, and Methods of Using Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,421-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
TELEFAX: 201-683-4117

20030165806

; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 426 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-816-011-45

Query Match 98.2%; Score 2062; DB 12; Length 426;
 Best Local Similarity 98.5%; Pred. No. 1.2e-199;
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
 :|||||
 DB 16 VAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 75
 QY 61 GATVFALDQPHIEISORTTIVIOKOTFISQHSQVNSTELDIIQIVAAINAGIIPLGNT 120
 :|||||
 DB 76 GATVFALDQPHIEISORTTIVIOKOTFISQHSQVNSTELDIIQIVAAINAGIIPLGNT 135
 QY 121 SNOISHMDLSSFFPAGTIVTTIGFQNISPRTEGKIFCIITVALLGIPFGFLLAGVDQ 180
 :|||||
 DB 136 SNOISHMDLSSFFPAGTIVTTIGFQNISPRTEGKIFCIITVALLGIPFGFLLAGVDQ 195
 QY 181 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 240
 :|||||
 DB 196 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 255
 QY 241 AIFVAVITLTITGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVRVIS 300
 :|||||
 DB 256 AIFVAVITLTITGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVRVIS 315
 QY 301 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
 :|||||
 DB 316 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 375
 QY 361 ELTPCRRTLNVNLTNERDVLPLPLKTESIYNGLTPHCAGEEIAVENIK 411
 :|||||
 DB 376 ELTPCRRTLNVNLTNERDVLPLPLKTESIYNGLTPHCAGEEIAVENIK 426

RESULT 7
US-08-816-011A-45

; Sequence 45, Application US/08816011A
 ; GENERAL INFORMATION:
 ; APPLICANT: Price, Laura A.
 ; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
 ; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Home Products Corporation
 ; STREET: One Campus Drive
 ; CITY: Parsippany
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07054
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,011A
 ; FILING DATE: 11-MAR-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Matthews, Gale F.
 ; REGISTRATION NUMBER: 32,269
 ; REFERENCE/DOCKET NUMBER: 32,421-C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-683-2134

; TELEFAX: 201-683-4117
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 426 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-816-011A-45

Query Match 98.2%; Score 2062; DB 12; Length 426;
 Best Local Similarity 98.5%; Pred. No. 1.2e-199;
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
 :|||||
 DB 16 VAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 75
 QY 61 GATVFALDQPHIEISORTTIVIOKOTFISQHSQVNSTELDIIQIVAAINAGIIPLGNT 120
 :|||||
 DB 76 GATVFALDQPHIEISORTTIVIOKOTFISQHSQVNSTELDIIQIVAAINAGIIPLGNT 135
 QY 121 SNOISHMDLSSFFPAGTIVTTIGFQNISPRTEGKIFCIITVALLGIPFGFLLAGVDQ 180
 :|||||
 DB 136 SNOISHMDLSSFFPAGTIVTTIGFQNISPRTEGKIFCIITVALLGIPFGFLLAGVDQ 195
 QY 181 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 240
 :|||||
 DB 196 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 255
 QY 241 AIFVAVITLTITGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVRVIS 300
 :|||||
 DB 256 AIFVAVITLTITGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVRVIS 315
 QY 301 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
 :|||||
 DB 316 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 375
 QY 361 ELTPCRRTLNVNLTNERDVLPLPLKTESIYNGLTPHCAGEEIAVENIK 411
 :|||||
 DB 376 ELTPCRRTLNVNLTNERDVLPLPLKTESIYNGLTPHCAGEEIAVENIK 426

RESULT 8

US-08-816-011C-45

; Sequence 45, Application US/08816011C
 ; GENERAL INFORMATION:
 ; APPLICANT: Price, Laura A.
 ; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
 ; TITLE OF INVENTION: AND METHODS OF USING SAME
 ; FILE REFERENCE: 01142, 0122 SEQUENCE LISTING
 ; CURRENT APPLICATION NUMBER: US/08/816,011C
 ; CURRENT FILING DATE: 1997-03-11
 ; PRIOR APPLICATION NUMBER: 08/332,312
 ; PRIOR FILING DATE: 1994-10-31
 ; PRIOR APPLICATION NUMBER: PCF/US95/14364
 ; PRIOR FILING DATE: 1995-10-25
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 45
 ; TYPE: PRT
 ; LENGTH: 426
 ; ORGANISM: Homo sapiens
 US-08-816-011C-45

Query Match 98.2%; Score 2062; DB 12; Length 426;
 Best Local Similarity 98.5%; Pred. No. 1.2e-199;
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
 :|||||

```

Db 16 VAAPDLDPKSAONSKRSLFSFKPTVYLASRVESDTTINVMKKTSTIFLVVLYLII 75
QY 61 GATVEKALEOPHEISORTTIVYOKOTFISSHSCVNSTELDELIOOYVAINAGIIPLGNT 120
Db 76 GATVEKALEOPHEISORTTIVYOKOTFISSHSCVNSTELDELIOOYVAINAGIIPLGNT 135
QY 121 SNOISHMWDGSSFFAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
Db 136 SNOISHMWDGSSFFAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 195
QY 181 LGTIFGKIAVEDETFIKMNVSOIKRIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 196 LGTIFGKIAVEDETFIKMNVSOIKRIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 255
QY 241 AIYEVVITLTITIGFDYVAGSDIEYDFKPYVMFWILVGLAFVAVLSMIGMLRVYS 300
Db 256 AIYEVVITLTITIGFDYVAGSDIEYDFKPYVMFWILVGLAFVAVLSMIGMLRVYS 315
QY 301 KKTKEEVEGFRAHAEMWTANTYAEFKETRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
Db 316 KKTKEEVEGFRAHAEMWTANTYAEFKETRRLSVEIYDKFORATSIKRLSAELAGNHQ 375
QY 361 ELTPCRRLSVNHLTNERDVLPLPKTESIYLNGLAPHCAGEIAVENIK 411
Db 376 ELTPCRRLSVNHLTNERDVLPLPKTESIYLNGLAPHCAGEIAVENIK 426

```

RESULT 9

US-09-503-089a-4

```

; Sequence 4, Application US/09503089a
; GENERAL INFORMATION:
; APPLICANT: PATEL, AMANDA J.
; APPLICANT: HONORE, ERIC
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMERY, GEORGES
; APPLICANT: LAZDUSKI, MICHEL
; TITLE OF INVENTION: A method for the identification of anesthetics
; FILE REFERENCE: F17B12prov3-humanantREK
; CURRENT APPLICATION NUMBER: US/09/503,089a
; CURRENT FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft word 2000
; SEQ ID NO 4
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-503-089a-4

```

Query Match 97.2%; Score 2041; DB 19; Length 411;

Best Local Similarity 96.1%; Pred. No. 1.6e-197;

Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MAAPDLDPKSAONSKRSLFSFKPTVYLASRVESDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLDPKSAONSKRSLFSFKPTVYLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVEKALEOPHEISORTTIVYOKOTFISSHSCVNSTELDELIOOYVAINAGIIPLGNT 120
Db 61 GATVEKALEOPHEISORTTIVYOKOTFISSHSCVNSTELDELIOOYVAINAGIIPLGNT 120
QY 121 SNOISHMWDGSSFFAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
Db 121 SNOISHMWDGSSFFAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
QY 181 LGTIFGKIAVEDETFIKMNVSOIKRIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKIAVEDETFIKMNVSOIKRIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYEVVITLTITIGFDYVAGSDIEYDFKPYVMFWILVGLAFVAVLSMIGMLRVYS 300
Db 241 AIYEVVITLTITIGFDYVAGSDIEYDFKPYVMFWILVGLAFVAVLSMIGMLRVYS 300

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QY 301 KKTKEEVEGFRAHAEMWTANTYAEFKETRRLSVEIYDK 360
Db 301 KKTKEEVEGFRAHAEMWTANTYAEFKETRRLSVEIYDK 360
QY 361 ELTPCRRLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVENIK 411
Db 361 ELTPCRRLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVENIK 411

```

RESULT 10

US-09-828-746-6

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; Sequence 6, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

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Query Match 96.9%; Score 2035; DB 19; Length 411;

Best Local Similarity 95.9%; Pred. No. 6.3e-197;

Matches 394; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAONSKRSLFSFKPTVYLASRVESDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLDPKSAONSKRSLFSFKPTVYLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVEKALEOPHEISORTTIVYOKOTFISSHSCVNSTELDELIOOYVAINAGIIPLGNT 120
Db 61 GATVEKALEOPHEISORTTIVYOKOTFISSHSCVNSTELDELIOOYVAINAGIIPLGNT 120
QY 121 SNOISHMWDGSSFFAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
Db 121 SNOISHMWDGSSFFAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
QY 181 LGTIFGKIAVEDETFIKMNVSOIKRIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKIAVEDETFIKMNVSOIKRIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYEVVITLTITIGFDYVAGSDIEYDFKPYVMFWILVGLAFVAVLSMIGMLRVYS 300
Db 241 AIYEVVITLTITIGFDYVAGSDIEYDFKPYVMFWILVGLAFVAVLSMIGMLRVYS 300
QY 301 KKTKEEVEGFRAHAEMWTANTYAEFKETRRLSVEIYDK 360
Db 301 KKTKEEVEGFRAHAEMWTANTYAEFKETRRLSVEIYDK 360
QY 361 ELTPCRRLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVENIK 411
Db 361 ELTPCRRLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVENIK 411

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RESULT 11

US-09-655-272-4

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; Sequence 4, Application US/09655272
; GENERAL INFORMATION:
; APPLICANT: HONORE, ERIC
; APPLICANT: FINK, MICHEL

```

0.447

APPLICANT: LAZDUNSKI, MICHEL
APPLICANT: LESAGE, FLORIAN
APPLICANT: DUPRAT, FABRICE
TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
FILE REFERENCE: 1383-00
CURRENT APPLICATION NUMBER: US/09/655,272
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/FR99/00404
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: FR 98/02725
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 370
TYPE: PR
ORGANISM: Unknown Sequence
FEATURE:
OTHER INFORMATION: Description of Unknown Sequence: TREK
US-09-655-272-4

Query Match 87.3%; Score 1833; DB 20; Length 370;
Best Local Similarity 96.7%; Pred. No. 1.7e-176;
Matches 356; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAONSKPRLSSTKPTVLASRVESDPTTNVKKMTVSTFLVVLXLI 60
DB 1 MAAPDLDPKSAONSKPRLSSTKPTVLASRVESDPTTNVKKMTVSTFLVVLXLI 60
OY 61 GAATFALDQPHISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
DB 61 GAATFALDQPHISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
OY 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALGIPLEGFLAGVGDO 180
DB 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALGIPLEGFLAGVGDO 180
OY 181 LGTFEGKIAKVEDPFIKNNVSTKIRIISTIFIFGCVLPAVAFKHEGMSALD 240
DB 181 LGTFEGKIAKVEDPFIKNNVSTKIRIISTIFIFGCVLPAVAFKHEGMSALD 240
OY 241 AIFGVYITLTITGFGDYVAGSDIEYDFKPYVWFMIILGLAFPAVLSMIGDMLRVIS 300
DB 241 AIFGVYITLTITGFGDYVAGSDIEYDFKPYVWFMIILGLAFPAVLSMIGDMLRVIS 300
OY 301 KTKKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGLNHNO 360
DB 301 KTKKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGLNHNO 360
OY 361 ELTPCART 368
DB 361 ELTPCART 368

RESULT 12

US-09-144-914-8
Sequence 8, Application US/09144914
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989, 6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234

EARLIER FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PR
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: TREK-1
US-09-144-914-8

Query Match 86.9%; Score 1824; DB 1; Length 370;
Best Local Similarity 96.5%; Pred. No. 1.3e-175;
Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAONSKPRLSSTKPTVLASRVESDPTTNVKKMTVSTFLVVLXLI 60
DB 1 MAAPDLDPKSAONSKPRLSSTKPTVLASRVESDPTTNVKKMTVSTFLVVLXLI 60
OY 61 GAATFALDQPHISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
DB 61 GAATFALDQPHISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
OY 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALGIPLEGFLAGVGDO 180
DB 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALGIPLEGFLAGVGDO 180
OY 181 LGTFEGKIAKVEDPFIKNNVSTKIRIISTIFIFGCVLPAVAFKHEGMSALD 240
DB 181 LGTFEGKIAKVEDPFIKNNVSTKIRIISTIFIFGCVLPAVAFKHEGMSALD 240
OY 241 AIFGVYITLTITGFGDYVAGSDIEYDFKPYVWFMIILGLAFPAVLSMIGDMLRVIS 300
DB 241 AIFGVYITLTITGFGDYVAGSDIEYDFKPYVWFMIILGLAFPAVLSMIGDMLRVIS 300
OY 301 KTKKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGLNHNO 360
DB 301 KTKKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGLNHNO 360
OY 361 ELTPCART 368
DB 361 ELTPCART 368

RESULT 13

US-09-436-265-8
Sequence 8, Application US/09436265
GENERAL INFORMATION:
APPLICANT: REYES, ROBERTO
APPLICANT: DUPRAT, FABRICE
APPLICANT: LESAGE, FLORIAN
APPLICANT: FINK, MICHEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: FARMAN, NICOLETTE
APPLICANT: LAZDUNSKI, MICHEL
TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR
TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF
FILE REFERENCE: 1201-CIP2-00
CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/107,692
PRIOR FILING DATE: 1996-11-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 370
TYPE: PR

11/9/98
not
996

ORGANISM: Murine sp.
FEATURE:
OTHER INFORMATION: TREK-1
US-09-436-265-8

Query Match 86.9% Score 1824; DB 18; Length 370;
Best Local Similarity 96.3%; Pred. No. 1.3e-175;
Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAADLLDPKSAONSKPRLSFSTKPTVLASRVSDPTINVMKKKTVSTIPLVVVLII 60
DB 1 MAADLLDPKSAONSKPRLSFSTKPTVLASRVSDPTINVMKKKTVSTIPLVVVLII 60
QY 61 GATVFKALQEPHEISQRTTIVIQKOTFISQHSQVNSTELDELIOQIYAAINAGIIPLGNT 120
DB 61 GATVFKALQEPHEISQRTTIVIQKOTFISQHSQVNSTELDELIOQIYAAINAGIIPLGNS 120
QY 121 SNOISHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIIYALLGIPLFGFLLAGVGDQ 180
DB 121 SNOISHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIIYALLGIPLFGFLLAGVGDQ 180
QY 181 LGTFEGKIAKVEDFTFKMNVSOQTKIRIISTIFLFGCVLFVALPAIIFKHGWSALD 240
DB 181 LGTFEGKIAKVEDFTFKMNVSOQTKIRIISTIFLFGCVLFVALPAIIFKHGWSALD 240
QY 241 AIYFVVTITLTIGFGDVAGSDIEYDFYKPVVFWILVGLAFYFAVLSMIGMLRVIS 300
DB 241 AIYFVVTITLTIGFGDVAGSDIEYDFYKPVVFWILVGLAFYFAVLSMIGMLRVIS 300
QY 301 KKTKEEVEGFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360
DB 301 KKTKEEVEGFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360
QY 361 ELTPCRRT 368
DB 361 ELTPCRMT 368

RESULT 14
PCT-US01-14965-73
Sequence 73. Application PC/TUS0114965
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Roberts, Steven L.
APPLICANT: Benjamin, Christopher
APPLICANT: Karnovsky, Alla M.
APPLICANT: Ruble, Cara L.
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00133.PCT1
CURRENT APPLICATION NUMBER: PCT/US01/14965
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,526
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/216,893
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/223,245
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn version 3.0
SEQ ID NO 73
LENGTH: 543
TYPE: PRT

ORGANISM: Homo sapiens
PCT-US01-14965-73

Query Match 59.2% Score 1243; DB 18; Length 543;
Best Local Similarity 62.7%; Pred. No. 1.9e-11; Indels 28; Gaps 6;
Matches 247; Conservative 54; Mismatches 5; Indels 28; Gaps 6;

QY 2 AAPDLLPKSA-----AONSKPRLSFSTKPTVLASRVSDPTINVMKKKTVSTI 50
DB 22 AAAPVQCPKSAATNQPPAPAPPTPPRLSSIRATVVA-FPGTSGGGLQYVMKKKTVYAI 80
QY 51 FLVVVLIIIGATVFKALQEPHEISQRTTIVIQKOTFISQHSQVNSTELDELIOQIYAAI 110
DB 81 FVVVVVVLVGLVFRALQEPFESSOKNTIALERAEFLRIVCVSPOBELTLLIOHALDAD 140
QY 111 NAGIIPLGNTSNOISHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIIYALLGIPLF 170
DB 141 NAGVSPIGNSSSHMDLGSAPFFACTVTTTIGYGNIA STEGKIFCIIYALLGIPLF 200
QY 171 GFLLAGVGDQGTTFEGKIAKVEDFTFKMNVSOQTKIRIISTIFLFGCVLFVALPAIIF 230
DB 201 GFLLAGVGDQGTTFEGKIAKVEDFTFKMNVSOQTKIRIISTIFLFGCVLFVALPAIIF 260
QY 231 KHIEGWSALDAIYFVVTITLTIGFGDVAGG-SDIEYDFYKPVVFWILVGLAFYFAVL 289
DB 261 KYIEGWSALDAIYFVVTITLTIGFGDVAGGAGNAGINREK-KPLVFWILVGLAFYFAVL 320
QY 290 SMIDMLRVISKKTKEEVEGFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRL 349
DB 321 SMIDMLRVISKKTKEEVEGFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRL 378
QY 350 LSAELAGNHQDELTPCRRTLSVNLITNEDRVLP 383
DB 379 -SME-----RRRLGIDQRAHSLDMLSP 399

RESULT 15
US-09-852-386-73
Sequence 73. Application US/09852386
GENERAL INFORMATION:
APPLICANT: Roberts, Steven L.
APPLICANT: Benjamin, Christopher
APPLICANT: Karnovsky, Alla M.
APPLICANT: Ruble, Cara L.
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00133.US1
CURRENT APPLICATION NUMBER: US/09/852,386
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,526
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/216,893
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/223,245
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn version 3.0
SEQ ID NO 73
LENGTH: 543
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-386-73

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 16:57:36 : Search time 28.01 Seconds
(without alignments)
302.129 Million cell updates/sec

Title: US-09-503-089a-2
Perfect score: 2100
Sequence: 1 MAAPDLDPKSAQNSKPRRL.....LNGLPHCAGEIAVENIK 411

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/prodata/2/1aa/5b_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6a_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6b_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	4	US-09-236-080-2
2	2035	96.9	411	4	US-09-236-080-6
3	547	26.0	107	4	US-09-236-080-4
4	379.5	18.1	336	3	US-08-749-816-2
5	291.5	13.9	618	1	US-08-332-312-2
6	221	10.5	336	1	US-08-332-312-4
7	179	8.5	333	3	US-08-749-816-3
8	160.5	7.6	347	3	US-08-749-816-3
9	120	5.7	676	4	US-09-135-021-2
10	103.5	4.9	581	4	US-09-135-021-80
11	99.5	4.7	831	2	US-08-677-734A-11
12	99.5	4.7	834	2	US-08-677-734A-9
13	99.5	4.7	834	2	US-08-677-734A-10
14	97.5	4.6	832	2	US-08-677-734A-12
15	96.5	4.6	1036	2	US-08-720-484A-5
16	96.5	4.6	1036	4	US-08-953-823A-5
17	94.5	4.5	548	3	US-08-903-139B-28
18	94	4.5	535	3	US-08-286-870A-6
19	94	4.5	648	3	US-08-286-870A-4
20	94	4.5	719	3	US-08-286-870A-8
21	93.5	4.5	626	2	US-08-956-242-2
22	93.5	4.5	626	3	US-09-351-215-2
23	93.5	4.5	1159	2	US-08-956-242-13
24	93.5	4.5	1159	3	US-09-351-215-13
25	93.5	4.5	1159	4	US-09-226-012-2
26	93.5	4.5	1159	4	US-09-226-012-4
27	93	4.4	606	3	US-08-620-077B-3

28	92.5	4.4	473	1	US-08-597-236-	Sequence 13, Appl
29	92.5	4.4	543	1	US-08-746-682A	Sequence 13, Appl
30	91.5	4.4	548	3	US-08-903-139B	Sequence 9, Appl
31	91	4.3	888	2	US-08-956-242-1	Sequence 4, Appl
32	91	4.3	888	3	US-09-351-215-6	Sequence 4, Appl
33	90.5	4.3	547	3	US-08-903-139B-	Sequence 7, Appl
34	90.5	4.3	550	4	US-08-637-823B-1	Sequence 30, Appl
35	90	4.3	552	3	US-09-111-752-7	Sequence 7, Appl
36	89.5	4.3	1872	6	5386025-6	Sequence 4, Appl
37	88.5	4.2	483	4	US-08-637-823B-4	Sequence 4, Appl
38	88	4.2	548	2	US-08-637-823B-1	Sequence 5, Appl
39	88	4.2	548	2	US-08-676-279-5	Sequence 50, Appl
40	88	4.2	548	3	US-08-903-139B-	Sequence 8, Appl
41	88	4.2	548	4	US-08-637-823B-	Sequence 25, Appl
42	87.5	4.2	436	6	5432081-10	Sequence 7, Appl
43	87.5	4.2	482	4	US-08-637-823B-3	Sequence 32, Appl
44	87.5	4.2	484	4	US-08-637-823B-2	Sequence 2, Appl
45	87	4.1	548	1	US-07-675-211-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1	US-09-236-080-2	Application us/09236080
Sequence 2, Appl	Patent No. 6242217	
GENERAL INFORMATION:		
APPLICANT:	Helen Meadows	
APPLICANT:	Conrad Chapman	
TITLE OF INVENTION:	No. 6242217el Compounds	
FILE REFERENCE:	GP30031	
CURRENT APPLICATION NUMBER:	us/09/236, 080	
CURRENT FILING DATE:	1999-01-25	
NUMBER OF SEQ ID NOS:	6	
SOFTWARE:	FastSeq for Windows Version 3.0	
SEQ ID NO 2		
LENGTH:	411	
TYPE:	PRT	
ORGANISM:	Homo sapiens	
US-09-236-080-2		
Query Match	99.8% Score 2095; Df	Length 411;
Best Local Similarity	99.8% Pred. No. 5e-2.	
Matches 410: Conservative	1; Mismatches	0; Indels 0; Gaps 0;
1	MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDPTT	MAAKTVSTFLVVLVLI 60
1	MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDPTT	MAAKTVSTFLVVLVLI 60
1	MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDPTT	MAAKTVSTFLVVLVLI 60
61	GATVFKALBPHEHSORTTIVYIKOTFISQHSVCNSTE	IOOYVAINAGIIPRGNT 120
61	GATVFKALBPHEHSORTTIVYIKOTFISQHSVCNSTE	IOOYVAINAGIIPRGNT 120
61	GATVFKALBPHEHSORTTIVYIKOTFISQHSVCNSTE	IOOYVAINAGIIPRGNT 120
121	SNQSHMDLSSFFACTVTTTIGFNMISPTREGKIFCI	LYAALGIPLEGFLLAGVDQ 180
121	SNQSHMDLSSFFACTVTTTIGFNMISPTREGKIFCI	LYAALGIPLEGFLLAGVDQ 180
121	SNQSHMDLSSFFACTVTTTIGFNMISPTREGKIFCI	LYAALGIPLEGFLLAGVDQ 180
181	LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILEGC	LFVALPAILFKHIEGMSALD 240
181	LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILEGC	LFVALPAILFKHIEGMSALD 240
181	LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILEGC	LFVALPAILFKHIEGMSALD 240
241	AIYFVVTITLTIGGDDVAGSDIEYDFKPPVWEMILVC	AVFAAVLSMIGMLFVVIS 300
241	AIYFVVTITLTIGGDDVAGSDIEYDFKPPVWEMILVC	AVFAAVLSMIGMLFVVIS 300
241	AIYFVVTITLTIGGDDVAGSDIEYDFKPPVWEMILVC	AVFAAVLSMIGMLFVVIS 300
301	KKTKEEVEGFRRAHAEMTANTVAFKETRRLSVEIDKF	FMATSIKRLSAELAGHNO 360
301	KKTKEEVEGFRRAHAEMTANTVAFKETRRLSVEIDKF	FMATSIKRLSAELAGHNO 360
301	KKTKEEVEGFRRAHAEMTANTVAFKETRRLSVEIDKF	FMATSIKRLSAELAGHNO 360
361	ELAPCRFTLSVNLITNERDVLPIILKTESIYLANGLP	HCJIAVENIK 411
361	ELAPCRFTLSVNLITNERDVLPIILKTESIYLANGLP	HCJIAVENIK 411
361	ELAPCRFTLSVNLITNERDVLPIILKTESIYLANGLP	HCJIAVENIK 411

Db 361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

RESULT 2

US-09-236-080-6

Sequence 6, Application US/09236080

Patent No. 6242217

GENERAL INFORMATION:

APPLICANT: Helen Meadows

APPLICANT: Conrad Chapman

TITLE OF INVENTION: No. 6242217el Compounds

FILE REFERENCE: GP30031

CURRENT APPLICATION NUMBER: US/09/236,080

CURRENT FILING DATE: 1999-01-25

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6

LENGTH: 411

TYPE: PRT

ORGANISM: Mus musculus

US-09-236-080-6

Query Match 96.9%; Score 2035; DB 4; Length 411;
Best Local Similarity 95.9%; Pred. No. 6.9e-200;
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

1 MAAPDLDPKSAONSKPRLSFSKPTVLASRYESDPTIIVMKTKVSTFLVVLIT 60

1 MAAPDLDPKSAONSKPRLSFSKPTVLASRYESDPTIIVMKTKVSTFLVVLIT 60

61 GATVFKALPEPHISORTTIVIOKOTFISOHSCVNSTEDELIIQIIVAAINAGIPLGNT 120

61 GATVFKALPEPHISORTTIVIOKOTFISOHSCVNSTEDELIIQIIVAAINAGIPLGNT 120

61 GAUVFKALPEPHISORTTIVIOKOTFISOHSCVNSTEDELIIQIIVAAINAGIPLGNT 120

121 SNOISHMDLSSFFPACTVITTTGFGNISPTREGKIFCIIVALLGIPFLAGVGDQ 180

121 SNOISHMDLSSFFPACTVITTTGFGNISPTREGKIFCIIVALLGIPFLAGVGDQ 180

181 LGTFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 240

181 LGTFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 240

241 AIYFVVITLTIGFGDYVAGSDIEYLFKPYVWFILVGLAYFAVLSMIDWLRVIS 300

241 AIYFVVITLTIGFGDYVAGSDIEYLFKPYVWFILVGLAYFAVLSMIDWLRVIS 300

301 KTKKEVGEFRAAAEYTAVTAEFKETRRRLSVEIYDKFORATSVKRLSABLACNHNQ 360

301 KTKKEVGEFRAAAEYTAVTAEFKETRRRLSVEIYDKFORATSVKRLSABLACNHNQ 360

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

361 ELTPCRRRTLSVNHLSRBDVLPPLLTKESTIYLNGLPHPCAGEEIAVENIK 411

US-09-236-080-4

Query Match 26.0%; Score 547; DB 1; Length 107;

Best Local Similarity 98.1%; Pred. No. 1.5e-8;

Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

119 NTSNOISHMDLSSFFPACTVITTTGFGNISPTREGKIFCIIVALLGIPFLAGV 178

119 NTSNOISHMDLSSFFPACTVITTTGFGNISPTREGKIFCIIVALLGIPFLAGV 178

1 NTSNOISHMDLSSFFPACTVITTTGFGNISPTREGKIFCIIVALLGIPFLAGV 178

1 NTSNOISHMDLSSFFPACTVITTTGFGNISPTREGKIFCIIVALLGIPFLAGV 178

179 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

179 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

61 DQGTIFGKGIKVEDTIFKMWVSOTKIRIITIIIFLFGCVLFAVLPPIIFKHIEGMSALD 225

DB 85 ASNGSVLSVSNASGN-NMWDFTSALFFASTVLSITGGHVTPLSDGKAFCLITSVIGIP 143
QY 169 LFGCLAGVGDGDLITFGKJIAKVEDFTFKNNVOTKIRIISTII--FIIIGCVLVALP 226
DB 144 FTLEFLAVVORIVVHTR--RPVLYFIIRKGFSGKOVAYIAHVALLGFAVTSCEFFI--P 199
QY 227 AIIKHEIE-GMSALDAIVFVITLTITIGFDGVAG-GSDIEYLDYFKPVVFWIIVGLAY 284
DB 200 AAFSVLEDDMNFLSEFECFISLTIGLDYVPEGYNQKFRRELYKIGIICYLLGLIA 259
QY 285 FAALVSHIGMLRYISK-----KTKEVGEFRRAHAE 316
DB 260 MLVVFETFE-LHELKFRKMFYVKDKDEQVHIIE 295

RESULT 5
US-08-332-312-2
Sequence 2, Application US/08332312
Patent No. 5559026

GENERAL INFORMATION:
APPLICANT: Price, Laura A.
TITLE OF INVENTION: Functional Expression of a Drosophila
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: US
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332.312
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: P-38,711
REFERENCE/DOCKET NUMBER: 32,421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-312-2

Query Match 13.9%; Score 291.5; DB 1; Length 618;

Best Local Similarity 27.8%; Pred. No. 2.8e-21;
Matches 88; Conservative 64; Mismatches 123; Indels 41; Gaps 13;

QY 50 IFVLVVLVLLIGATVFALEQPHRE---ISORTIIVIGKOTFFISOHSOVNSTELDELIOQ 105
DB 9 LLIIVISILMGALIIYHIEGEEKISAEQRKQAIANELELDGDKNTTODEIIQR 68
QY 106 IVAAIMAGIIPLGNTSNOISHWLGSSEFFAGVYITIGFNGISPRTEGKIFCIYALL 165
DB 69 ISDVCGRKVTLPPTYDDPPTWTFYHAFVAFVCSFVGYCNISPTTFAGMIMIAVSVI 128
QY 166 GIPLEPFLAGVGDGDLITFGKJIAKVEDFTFKNNV-----QTKIRIISTIIIFILE-G 218
DB 129 GIPVNGIIFAG-----LGEYFGRTFEAIVRYRYKMYKMDHMYVPOLGLITTVIIVALIPG 184

QY 219 CVLFPALPAI---IFKHEGMSALDAIVFVITLTITIGFGRVVA-----GSDIE 265
DB 185 IALFLVLPVGVHLLREL-GLSSI-SLYSVYTTTIGFCIVVPTFGANQKREGGMEV 242
QY 266 YLDYFKPVVFWIIVGLAIFAAVLSMIGMLRYISK--KKEVGEFRRAHAEVIANV 321
DB 243 YQIVV--IWMF--IFSLGYLVIMTFTTRGLQ--SKRL--GLSSNLKATONRIMSGV 296
QY 322 TAEFKETRRRLSVEIY 337
DB 297 TKDVGILRRMLN-ELY 311

RESULT 6
US-08-332-312-4
Sequence 4, Application US/08332312
Patent No. 5559026

GENERAL INFORMATION:
APPLICANT: Price, Laura A.
TITLE OF INVENTION: Functional Expression of a Drosophila
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: US
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332.312
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: P-38,711
REFERENCE/DOCKET NUMBER: 32,421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-312-4

Query Match 10.5%; Score 221; DB 1; Length 336;

Best Local Similarity 26.2%; Pred. No. 1.8e-11;
Matches 59; Conservative 37; Mismatches 10; Indels 52; Gaps 6;

QY 120 TSNQISH-----WDLGSSEFFAGVYITITIGFNGISPRTH--KIFCIYALLGIPLEFL 173
DB 15 TSNEVKKNAATEMTWTFSSIFFAVTVTTTIGGNBPVPTNIBRMCLFSLGIPL--T 71
QY 174 LAGVGDLGTIFGKJIAKVEDFTFK-----WNSQT 204
DB 72 LVTIADLAGKLSHLWLVGNLYLKLXYLLISRRRKERR--CECHSHGSHDMNTEER 131
QY 205 KIRIISTIIIFLCVFLVALPALIIFKHIEGMSALDAIY--VITLTIGFDGVAGGSDI 264
DB 132 RI-----PAFLVALIIVTAAAGVLSMKLEPWSFTSTYR--ITMTTVGFGDMLPRDGY 187
QY 265 EYIDF-----YKPVVFWIIVGLAIFAAVLSMIG-MLRYI 299

Db 188 MYIIILYIIIGKFSMKKOKFIPLGLAITTCMDIIVGVOYIRKI 232

RESULT 7

US-08-749-816-4
Sequence 4, Application US/08749816
Patent No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunkl, Michel
APPLICANT: Romey, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
CLASSIFICATION: 336
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989,6351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-4

Query Match 8.5%; Score 179; DB 3; Length 383;
Best Local Similarity 24.3%; Pred. No. 4.4e-10;
Matches 74; Conservative 45; Mismatches 94; Indels 92; Gaps 14;

QY 50 IELVVLIIIGATVKALEPHIEISORTIIVIOKOTFISQHSVCNSTELDELIOQIVAA 109
DB 44 LVISCVTYALGAYLPLSLIHPELKRREKAI-----REFQDKQOFMGN 88
QY 110 INAG-----IIPLGNTSNO-----ISH-----MDLGSFEAGTVIT 141
DB 89 ITSGIENSESIFITTKKLLIMLEDAHNAHAFEFELNHEIPDMNTFSSALVFTTTTIV 148
QY 142 TIGFGNISPTREGKIFLCIIVALLGIPLEFGELLAVGD---QLGTTFGKGIARVEDTFIK 198
DB 149 PVGYGIPTPVSAGRMCLIVALLGIPLVITMADTGKFAQLVT-----R 194
QY 199 W-----VNSQKRIIISTIIIFILFCVLFVALPAI---IFKHIGSALDAIYFVITLT 251
DB 195 WFGDNMA-----IPALIFV---CLLF-AVPLVGFILCSTNITVYLDVSFSLSTIFT 244

QY 252 IGFQDVAGSGDIEYDFKPVVWFILVGLAFVAFVLSFG---DMLRVISK---KTK 304
DB 245 IGFQDLPLPDNNVIAHVLFE-----LAVGVLVTTTLQ:VAEMIDRVHYMRHVGKAK 296

QY 305 EEVGE 309
DB 297 ELAKG 301

RESULT 8

US-08-749-816-3
Sequence 3, Application US/08749816
Patent No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunkl, Michel
APPLICANT: Romey, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
CLASSIFICATION: 336
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989,6351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-3

Query Match 7.6%; Score 160.5; Length 347;
Best Local Similarity 24.1%; Pred. No. 3e-07;
Matches 58; Conservative 52; Mismatches 97; Indels 43; Gaps 10;

QY 52 LVVVLIIIGATVKALEPHIEISORTIIVIOKOTFIS:VNSTELDELIOQIVAAIN 111
DB 44 ITLVFNLIIGAGIEYLAE-----TONSSSLNENSFVSK-CLHNPIC--GKTTAEKK 93
QY 112 AGIIPGNTSNOISQHSMD-LGSSFEAGTVITIGFNIISPTREGKIFLCIIVALLGIP 169
DB 94 S---KIGKCLTSSRIIDGKALFESWTIXSTVGYSLIPHSILGVLITFTSLMIRPV 150
QY 170 -----FGELLAGVGDQIGTIFGKGIARVEDTFIKWNSQFKIRIIST-----IIFT 215
DB 151 IAKFEEGTFLAHF---LVVVSNTRLAVKAKAYKLSQW:EVNAETPSNSLQHDYILFLSS 207

QY 216 LFGCVLPAALIEFKHIEGMSALDAIYFVITLTITIGFDYVAGGSDIEYDEKPYW 275
 Db 208 LLCSISILSSALFSSISENISYSSVFGITITFLIGIGIVP7N-----LWV 256
 QY 276 F 276
 Db 257 F 257

RESULT 9

US-09-135-021-2
 ; Sequence 2, Application US/09135021A
 ; Patent No. 6150104
 ; GENERAL INFORMATION:
 ; APPLICANT: Splawski, Igor
 ; APPLICANT: Keating, Mark T.
 ; TITLE OF INVENTION: A HOMOLOGOUS MUTATION IN KVLQ1 WHICH CAUSES JERVELL
 ; FILE REFERENCE: 2323-128
 ; CURRENT APPLICATION NUMBER: US/09/135,021A
 ; EARLIER FILING DATE: 1998-08-17
 ; EARLIER APPLICATION NUMBER: 08/874,655
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/094,477
 ; EARLIER FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 676
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-135-021-2

Query Match 5.7%; Score 120; DB 4; Length 676;
 Best Local Similarity 19.4%; Pred. No. 0.0011;
 Matches 90; Conservative 70; Mismatches 137; Indels 166; Gaps 24;

QY 2 AAPDL---LDPKSAONSKPRLS-FSTRPVLASRVESDTINMK-----KTV---STI 50
 Db 71 AAPVASDLGRPPV-SIDRPVSTYSTRPVLAITHOGRVYNLEPRTGKCEVYHFAV 129
 QY 51 FLVVVLLIGATVFKALEOPHEISORTTIVIOKOTFISQHCNVSTELDELIOIYVAI 110
 Db 130 FLIVLVCLIF--SVLSTIEOYALALATGTFWM-----EIVLVV 165
 QY 111 NAGIIPGNTSNQISHMDLGSSFFAG-----TVITTTIGFN 147
 Db 166 FFG-----TEYVVRMLMSAGCRSKYVGLMGRLREARKPISIIDLIYVAVSMVLCVG--- 216
 QY 148 ISPTGEGKICFIYALIGFLPFGFL-LAGVGDGLTIFGKIAKVEDTFIKMNVSOIKI 206
 Db 217 -----SKQVRA-TSAIRGIRFLOILRLHVDROGGT-----W----- 248
 QY 207 RIISTITFI--LFGCVLPAALIEFK-----HIEGMSALDAIYFVI 247
 Db 249 RLDSVVEIHRQELITLTYIGFLGIFSSYFVLAEKDAVNESGVEGSAADLMMGV 308
 QY 248 TLTTIGREDYVAGSDIEYDFYKPVWF-----MLVGLAFYAAVLSMIGDM--LRV 298
 Db 309 TTTTIGYGDVY-----POTWVGKTIASCFVSFAISFPALPAGILGSGFALKV 355
 QY 299 ISKTKKEVGE-----FRAHAAE-----WTANTYAEKRETRRLSVEIYK 340
 Db 356 QOKOROKHFNQIIPAAASLIOTANRCYAAENPDSSTWKIYIR--KAPRSHTLISPSK 412
 QY 341 QRAFSIKRRLSAGLGNHNOELTPCQRTLSVNHNLTERNDVLP 383
 Db 413 KKSYYVKKK---KFLDKDNGVTGEEKMLVPHITCD---PP 448

RESULT 10

US-09-135-021-80
 ; Sequence 80, Application US/09135021A
 ; Patent No. 6150104
 ; GENERAL INFORMATION:
 ; APPLICANT: Splawski, Igor
 ; APPLICANT: Keating, Mark T.
 ; TITLE OF INVENTION: A HOMOLOGOUS MUTATION IN KVLQ1 WHICH CAUSES JERVELL
 ; FILE REFERENCE: 2323-128
 ; CURRENT APPLICATION NUMBER: US/09/135,021A
 ; EARLIER FILING DATE: 1998-08-17
 ; EARLIER APPLICATION NUMBER: 08/874,655
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/094,477
 ; EARLIER FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 80
 ; LENGTH: 581
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-135-021-80

Query Match 4.9%; Score 103.5; DB 4; Length 581;
 Best Local Similarity 18.4%; Pred. No. 0.043;
 Matches 76; Conservative 62; Mismatches 118; Indels 157; Gaps 20;

QY 44 WKTV---STIFLVVLLIIGATVFKALEOPHEISORTTIVIOKOTFISQHCNVSTELD 100
 Db 25 WKCEVYHFAVFLIVLCIF--SVLSTIEOYALALATGTFWM----- 64
 QY 101 ELIOQIVAAINAGIIPGNTSNQISHMDLGSSFFAG----- 137
 Db 65 -----EIVLVVFC-----TEYVVRMLMSAGCRSKYVGLMGRLREARKPISIIDLIYVAVS 114
 QY 138 TVITTTIGFNISPTGEGKICFIYALIGFLPFGFL-LAGVGDGLTIFGKIAKVEDTF 196
 Db 115 MVLVCVG-----SKQVRA-TSAIRGIRFLOILRLHVDROGGT----- 152
 QY 197 IKMNVSOIKIRIISTITFI--LFGCVLPAALIEFK-----HIEGMS 237
 Db 153 -W-----RLDSVVEIHRQELITLTYIGFLGIFSSYFVLAEKDAVNESGVEGS 203
 QY 238 ALDAIYFVITLTITIGFDYVAGGSDIEYDFYKPVWF-----MLVGLAFYAAVLS 290
 Db 204 YADALMGVYVTTIGYDKV-----POTWVGKTIASCFVSFAISFPALPAG 250
 QY 291 MIGDM--LRVISKTKKEVGE-----FRAHAAE-----WTANTYAEKRETR 330
 Db 251 ILGSGFALKVQOKORHFNQIIPAAASLIOTANRCYAAENPDSSTWKIYIR--KAPRS 307
 QY 331 RLSEIYDKFORAISIKRRLSAGLGNHNOELTPCQRTLSVNHNLTERNDVLP 383
 Db 308 HTLSPSPKPKRSYVKKK---KFLDKDNGVTGEEKMLVPHITCD---PP 353

RESULT 11

US-08-677-734A-11
 ; Sequence 11, Application US/08677734A
 ; Patent No. 5871919
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; TITLE OF INVENTION: Functional Analysis Of the Human Na+/H+ Exchanger Isoform,
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farbow, Warrtelt &
 ; ADDRESSSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,734A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387,0043-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-734a-11

Query Match 4.7% Score 99.5; DB 2; Length 831;
Best Local Similarity 19.0%; Pred. No. 0.19;

Matches 76; Conservative 65; Mismatches 105; Indels 155; Gaps 21;

QY 17 KPLRSESTKPTVL--ASRVESDPT-----INWKKRTVSIFLVVLYLLIGATVEKAL 68
DB 11 KPLALAAVAATSLRGVGRGIEEPNSGSGFQIVTFKHHVODPYIALMILV--ASLAKIV 68
QY 69 EOPHEISQRTIYQKOTFISQHSQVNSTELDELIOIVAINAGIIPRLNTSNOISHMD 128
DB 69 ---FHLSHKVTSVPEBALI-----VGLVLGGIV--WAADHIASFT 106
QY 129 LGSSEFF-----AGTVI--TTIGFNIISPTGEGKIFCIIVALL-----GIP 168
DB 107 LPTPLFEYLLPRLVLDAGYFMRNLFEGNL-----GTL--LLYAVIGIIMNAATIGLS 158
QY 169 LFGFLAGVDQGLTIFGKIAVEDTFIKWNSQTKIRIISTIFILFGCVLFEVALPA- 227
DB 159 LVGVFLISGL-----MGEIKIGLLD--FLLFGSLIAAADPVA 192
QY 228 -----IIFKHIEGMSALD-----AIYEVVITLTTIGRGDVVAGSGSIEVLDYF 270
DB 193 VLAFFEEVHNEVLTIVFESLINDAVTVLVNVESEVTLG--GDAVVG-----VDCV 245
QY 271 KPVVWMI-----LVGLAFAAVLSMIGDM--LRVI----- 299
DB 246 KGVISFEVVSLSGTIVGV--IFAPLLSLVTFRTKHVRRIIEGFEVVISLSYLSMELSTS 304
QY 300 -----SKTKREEVGEFRAHAAEWTAVNTAEFKET 328
DB 305 AIIAIFCGICCOKRYKANISEQSATTVRYTMKMLASGAET 345

RESULT 12

US-08-677-734a-9
Sequence 9, Application US/08677734a
Patent No. 5871919
GENERAL INFORMATION:
APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Donowitz, Mark
APPLICANT: Tse, Chung-Ming

TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of Human Na⁺/H⁺ Exchanger Isoform,
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Gertel &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,734A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387,0043-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-734a-9

Query Match 4.7% Score 99.5; DB 2; Length 834;
Best Local Similarity 20.4%; Pred. No. 0.19;

Matches 73; Conservative 64; Mismatches 73; Indels 127; Gaps 22;

QY 43 KKWTSIFLVVLYLLIGATVEKALEOPHEISQRTIYQKOTFISQHSQVNSTELDEL 102
DB 48 EMHVODPY-VIALMILVASLAKIGFHLHKV---TSVVFALLI----- 89
QY 103 IOQIVAINAGIIPRLNTSNOISHMDLGSSEFF-----AGTVI--TTIGFNIISPR 151
DB 90 ---VGLVLGGIV--WAADHIASFTLPTVEFFYLLPFT--DAGYFMRNLFEGNL--- 140
QY 152 TEGKIFCIIVALL-----GIPLFGFLAG--VGD--TTIGKIAKVEDTF 196
DB 141 ---GTL--LLYAVIGIIMNAATIGLSLVGVFLSGMLGDLTLDLGLSMAAYD----- 192
QY 197 IKWNSQTKIRIISTIFILFGCVLFEVALPAIFKHIEGMSAL-DAIYEVVITLTTIGRG 255
DB 193 -----PVAVLAVEEHNVEVLT-----IYF-----GSLINDAVTVLVN--PE 232
QY 256 DYVA--GSDIEYIDFTKPVVWMI-----LVGLAFAAVLSMIGDM--LRVI----- 299
DB 233 SFVALGDMVTGVCVKGVISFEVVSLSGTIVGV--FAPLLSLVTFRTKHVRRIIEGFEV 291
QY 300 -----SKTKREEVGEFRAHAAEWTAVNTAEFKET 328
DB 292 IISYLSYLSMELSLAIIAIFCGICCOKRYKANISEQSATTVRYTMKMLASGAET 348

RESULT 13

US-08-677-734a-10
Sequence 10, Application US/08677734a
Patent No. 5871919
GENERAL INFORMATION:
APPLICANT: Brant, Steven R.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 16:34:15 ; Search time 47.95 Seconds

(Without alignments)
519.634 Million cell updates/sec

Title: US-09-503-089a-2

Perfect score: 2100

Sequence: 1 MAAPDLDPKSAQNSKPRL.....LNGLTPHCAGEIAVENIK 411

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT.*
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4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT.*
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21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	AAV34133	Human potassium ch
2	2095	99.8	411	AAV28496	h-TREK1 polypeptid
3	2095	99.8	411	AAV50044	Human TREK, Homo
4	2035	96.9	411	AAV28497	Mouse h-TREK1 poly
5	1833	87.3	370	AAV30648	A mechanically sen
6	803	38.2	393	AAV94425	Human h-TRAAK poly
7	803	38.2	393	AAV94426	Human h-TRAAK poly
8	776.5	37.0	398	AAV30647	A mechanically sen
9	547	26.0	107	AAV28498	Partial h-TREK1 po
10	427	20.3	499	AAV90356	Human TWIK-2 prote
11	427	20.3	499	AAV79675	Human potassium ch

12	427	20.3	499	21	AAV94875	Human protein clon
13	391	18.6	332	21	AAV90354	Human TWIK-3 prote
14	382	18.2	361	22	AAV31805	Amino acid sequenc
15	379.5	18.1	336	18	AAV23397	TWIK-1 potassium c
16	379.5	18.1	336	21	AAV79673	Human potassium ch
17	363	17.3	394	21	AAV79674	Human potassium ch
18	363	17.3	394	21	AAV87291	Human signal pepti
19	349.5	16.6	374	21	AAV18807	Amino acid sequenc
20	349.5	16.6	374	21	AAV18813	Protein encoded by
21	348	16.6	313	20	AAV34132	Human potassium ch
22	348	16.6	313	20	AAV25116	Human hTREK-1 prot
23	348	16.6	313	21	AAV90355	Human TWIK-4 prote
24	348	16.6	313	21	AAV68737	KT4, a TWIK family
25	348	16.6	313	21	AAV68738	KT5, a TWIK family
26	337	16.0	405	21	AAV95230	Mouse potassium ch
27	309.5	14.7	408	22	AAV31804	Amino acid sequenc
28	291.5	13.9	618	17	AAV97984	DMORF1 potassium c
29	261.5	12.5	395	22	AAV31801	Amino acid sequenc
30	221.5	10.5	730	22	AAV31800	Amino acid sequenc
31	221	10.5	336	17	AAV97986	F22b7.7 potassium
32	209	10.0	995	22	AAV31799	Amino acid sequenc
33	179	8.5	383	21	AAV79677	Caenorhabditis ele
34	166.5	7.9	1153	22	AAV31802	Amino acid sequenc
35	160.5	7.6	347	21	AAV79676	Caenorhabditis ele
36	153.5	7.3	197	20	AAV34126	Human potassium ch
37	147.5	7.0	316	21	AAV34160	Arabidopsis thalia
38	147.5	7.0	316	21	AAV40370	Arabidopsis thalia
39	147.5	7.0	408	21	AAV14159	Arabidopsis thalia
40	147.5	7.0	408	21	AAV40369	Arabidopsis thalia
41	140.5	6.7	399	21	AAV41831	Arabidopsis thalia
42	140.5	6.7	424	21	AAV41830	Arabidopsis thalia
43	140.5	6.7	436	21	AAV41829	Arabidopsis thalia
44	139.5	6.6	248	21	AAV41461	Arabidopsis thalia
45	139.5	6.6	248	21	AAV40371	Arabidopsis thalia

ALIGNMENTS

RESULT	1	
AAV34133		
ID	AAV34133 standard: Protein: 411 AA.	
XX		
AC	AAV34133:	
XX		
DT	30-NOV-1999 (first entry)	
XX		
DE	Human potassium channel K+Hnov59.	
XX		
KM	Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;	
KW	cardiovascular disorder; CNS disorder; renal disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	W09943696-A1.	
XX		
PD	02-SEP-1999.	
XX		
PF	22-FEB-1999; 99MO-US03826.	
XX		
PR	19-JAN-1999; 99US-0116448.	
PR	25-FEB-1998; 98US-0076687.	
PR	07-AUG-1998; 98US-0095836.	
XX		
PA	(AXYS-) AXYS PHARM INC.	
PI	Curran ME, Hu P, Miller AP, Rutter M, Wang J;	
XX		
DR	WPI; 1999-527591/44.	
DR	N-PSDB; AA211915.	
XX		
PT	New nucleic acids encoding mammalian K+Hnov potassium channel proteins, useful for the diagnosis and treatment of episodic ataxia	

PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
 XX
 PS Claim 3; Page 104-105; 112pp: English.
 XX

CC This sequence represents the human K+Hnov59 potassium channel.
 CC K+Hnov proteins have a high degree of homology to known potassium
 CC channels and may be alpha subunits, which form the functional channel,
 CC or accessory subunits that act to modulate the channel activity. K+Hnov59
 CC is a 4 transmembrane domain, 2 pore domain potassium channel. The gene
 CC is located on chromosome 19, determined via PCR chromosome
 CC localisation using primers AA211939 and AA211940. K+Hnov cDNAs
 CC were isolated by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple
 CC independent clones. Potassium channels have critical roles in various
 CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS)
 CC disorders. Nucleotides encoding K+Hnov proteins may be used for
 CC identifying homologous or related proteins and the DNA sequences encoding
 CC them. They may be used to produce compositions that modulate the
 CC expression and function of the K+Hnov protein and in studying the
 CC biochemical pathways associated with it. They may also be used for the
 CC recombinant production of K+Hnov protein in fermentation cultures.
 CC Additionally, such nucleotides may be used in gene therapy protocols for
 CC the treatment of diseases associated with abnormal potassium channels.
 CC
 XX
 XX Sequence 411 AA:

Query Match 99.8%; Score 2095; DB 20: Length 411;
 Best Local Similarity 99.8%; Pred. No. 1.9e-209;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTINWMMKVTSTFLVVLVLI 60
 DB 1 maapdlldpksaansqnsprlsfstkptvlasrvesttinwmmkvtstflvvvlyli 60
 QY 61 GATVFALAEOPHEISQRTTIVIOKOFIISOHSCVNSTELDELIOQIVAAINAGIIPLGNT 120
 DB 61 gatvfalaeopheisqrttativioqkfisqhsncvnsteldelilqivaainagilpigt 120
 QY 121 SNOISHMDLGSFFPGTGTITGFGNISPRTEGKRECTIVALLGPIPLAGVGO 180
 DB 121 snqishmdlgssffgagvtitlgfgnisprrteggkrfctivallgpiplagvgdg 180
 QY 181 LGTIFSGIAKVEDTEIKMNSQTKIRIISTITFIIFGCVLFVALPAITFKHIEGMSALD 240
 DB 181 lgtifsgiakavedtefkwnvsqtkiristitfiifgcvlfvalpalitfkhegmsald 240
 QY 241 AITFVYITLTITFGDYVAGSGDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300
 DB 241 aifvyltltitfgdyvagsdleyldfkkpwwfwiwglavfaavlsimigdwlrvis 300
 QY 301 KKTKEEVEGEFRAHAEMTANVTAEFKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
 DB 301 kktkeevgefrhaaemtavtaefketrirrsveiydkfqratsikrlsaelaqnhq 360
 QY 361 ELTPCRRTLSVNHLTNERDVLPLPLKTESIYINGLTPHCAGEEIAVENIK 411
 DB 361 eltpcrrtlsvnhltnerdvlplplktestiyngltphcageelavienik 411

RESULT 2
 ID AA28496
 XX AA28496 standard; Protein; 411 AA.
 AC AA28496;
 XX
 DT 12-OCT-1999 (first entry)

XX h-TREK1 polypeptide.
 DE
 XX h-TREK1: two pore potassium channel; inflamm. v. nry disease;
 KW chromosome 1q32.
 XX
 OS Homo sapiens.
 XX
 PN M09937762-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 02-DEC-1998; 98WO-EP07805.
 XX
 PR 09-OCT-1998; 98GB-0022135.
 XX
 PR 27-JAN-1998; 98BP-0300570.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Chapman CG, Meadows HJ;
 PI
 DR WPI: 1999-469126/39.
 DR N-PSDB: AA200039.
 XX
 XX New two pore potassium channel used for, e.g., treatment of cancer,
 PT pulmonary, cardiovascular and inflammatory diseases
 XX
 PS Claim 3; Page 24; 44pp: English.

CC This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1
 CC polynucleotide AA200039. h-TREK1 is a two pore potassium channel, and
 CC the gene maps to human chromosome 1q32, between the markers D1937 and
 CC M15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
 CC disease or susceptibility to a disease related to expression or activity
 CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the
 CC treatment of diseases including cancer, pulmonary, cardiovascular, and
 CC inflammatory diseases, pain, psychiatric disorders including depression
 CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
 CC stroke, and head trauma and neurological disorders including migraine.

XX Sequence 411 AA:

Query Match 99.8%; Score 2095; DB 20: Length 411;
 Best Local Similarity 99.8%; Pred. No. 1.9e-209;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTINWMMKVTSTFLVVLVLI 60
 DB 1 maapdlldpksaansqnsprlsfstkptvlasrvesttinwmmkvtstflvvvlyli 60
 QY 61 GATVFALAEOPHEISQRTTIVIOKOFIISOHSCVNSTELDELIOQIVAAINAGIIPLGNT 120
 DB 61 gatvfalaeopheisqrttativioqkfisqhsncvnsteldelilqivaainagilpigt 120
 QY 121 SNOISHMDLGSFFPGTGTITGFGNISPRTEGKRECTIVALLGPIPLAGVGO 180
 DB 121 snqishmdlgssffgagvtitlgfgnisprrteggkrfctivallgpiplagvgdg 180
 QY 181 LGTIFSGIAKVEDTEIKMNSQTKIRIISTITFIIFGCVLFVALPAITFKHIEGMSALD 240
 DB 181 lgtifsgiakavedtefkwnvsqtkiristitfiifgcvlfvalpalitfkhegmsald 240
 QY 241 AITFVYITLTITFGDYVAGSGDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300
 DB 241 aifvyltltitfgdyvagsdleyldfkkpwwfwiwglavfaavlsimigdwlrvis 300
 QY 301 KKTKEEVEGEFRAHAEMTANVTAEFKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
 DB 301 kktkeevgefrhaaemtavtaefketrirrsveiydkfqratsikrlsaelaqnhq 360
 QY 361 ELTPCRRTLSVNHLTNERDVLPLPLKTESIYINGLTPHCAGEEIAVENIK 411
 DB 361 eltpcrrtlsvnhltnerdvlplplktestiyngltphcageelavienik 411

Db 361 eltpcrrtlsvnhltserdvlppllktesylnltpbcageelavlenlk 411

RESULT 3
ID AAB50044 standard; Protein: 411 AA.
X X AAB50044:
X X 19-MAR-2001 (first entry)
X X Human TREK.
X X DE Human TREK.
X X Human; TREK: 2P domain potassium channel; resting membrane potential;
X X neuronal excitability; neurotransmitter release modulation; epilepsy;
X X neurological disorder; sleep-related disorder; cognitive dysfunction;
X X attention deficit disorder; addiction; anxiety; phobia;
X X Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
X X erectile dysfunction; alopecia.
X X Homo sapiens.
X X OS
X X WO200072863-A2.
X X PN
X X 07-DEC-2000.
X X PD
X X 01-JUN-2000; 2000MO-GB02107.
X X PF
X X 01-JUN-1999; 99GB-0012733.
X X PR
X X (SMIK) SMITHKLINE BEECHAM PLC.
X X PA
X X Hervieu GJ, Meadows HJ, Randall AD;
X X PI
X X WPI: 2001-080422/09.
X X DR N-PSDB; AAC90412.
X X DR
X X Use of human TREK1 polypeptide, polynucleotides encoding them and
X X PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related
X X disorders, addition and dyskinesias including Parkinson's and
X X PT Huntington's chorea
X X PT
X X Claim 7; Page 29; 35pp; English.
X X PS
X X CC The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the
X X CC 2P domain potassium channel family of proteins which play a part in the
X X CC control of resting membrane potential. Modulation of these channels will
X X CC therefore affect neuronal excitability, thereby leading to a modulation
X X CC of neurotransmitter release and activity of neuronal networks. Such
X X CC modulation therefore may be useful for the treatment of certain
X X CC neurological conditions such as epilepsy, sleep-related disorders,
X X CC cognitive dysfunction, attention deficit disorder, addiction,
X X CC anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,
X X CC incontinence, erectile dysfunction or alopecia.
X X CC
X X SQ Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 22; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.9e-209;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAADLDLPKSAONSKPRLSFSTRPTVLASRVESDPTTINVMKKVTSTPLVVLVLI 60
Db 1 maepdlldpkksaonskprlsfstrptvlasrvesdpttinnvmkkvtstpllvvlyli 60

QY 61 GATVFKALEOPHEISQRTTIVIOKQTFISOHSCVNSTELDELIOOIVAAINAGIIPLGNT 120
Db 61 gatvfkaleqheisqrttllvqkqtfisqhsncvnsteldelilqivaaiaagilipngt 120

QY 121 SNOASHMDLGSSEFFAGVITTTGFGNISPRTEGKIFCIITIALGLPLGFFLLAGVGDQ 180
Db 121 snqshwdlgsseffagvtlttltgfnisprteggkifciliyalglplgffllagvgdq 180

QY 181 LGTIFGKGIANVEDTFFKMNVSQTKIRIISTIFILFGCVIVLPAIIFKHIGWSALD 240
Db 181 lgtlfgkgiakvedtffkwnvsqtkiristliffilfgcvlvalpaliffkhiegwsald 240

QY 241 AIFVAVITLTITIGRDYVAGSGDIEYDFKPPVWFMI; PLAVFAAVLSMIGMLRYS 300
Db 241 aifvavltltitigrdyvaagsdleyldfkrpwwfwj; plavyfaavlsmgmlrvis 300

QY 301 KKTKEEVEGFRAHAEMTANTAEFKETRRRLSVEIYDKFQFATSRKRSAAELAGNHQ 360
Db 301 kktkeevgefrhaaemtantaeftketrtrllsveiydkfqfatsrkksaaelagnhq 360

QY 361 ELTPCRRTLVSNHLTNERDVLPPLLKTESIYLNGLTPHCAGEELAVLENLK 411
Db 361 eltpcrrtlsvnhltserdvlppllktesylnltpbcageelavlenlk 411

RESULT 4
ID AAY28497 standard; Protein: 411 AA.
X X AAY28497:
X X AC
X X 12-OCT-1999 (first entry)
X X DT
X X Mouse h-TREK1 polypeptide.
X X DE
X X h-TREK1; two pore potassium channel; inflammatory disease;
X X KM chromosome 19q32.
X X KW
X X Mus musculus.
X X OS
X X WO9937762-A1.
X X PN
X X 29-JUL-1999.
X X PD
X X 02-DEC-1998; 98MO-EP07805.
X X PF
X X 09-OCT-1998; 98GB-0022135.
X X PR 27-JAN-1998; 98EP-0300570.
X X PA
X X (SMIK) SMITHKLINE BEECHAM PLC.
X X PA
X X Chapman CG, Meadows HJ;
X X PI
X X WPI: 1999-469126/39.
X X DR N-PSDB; AA200040.
X X DR
X X New two pore potassium channel used for, e.g., treatment of cancer,
X X PT pulmonary, cardiovascular and inflammatory
X X PT diseases
X X PT
X X Claim 3; Page 26; 44pp; English.
X X PS
X X This sequence is the mouse h-TREK1 polypeptide encoded by the h-TREK1
X X CC polynucleotide AA200040. h-TREK1 is a two pore potassium channel.
X X CC The polynucleotide sequence of h-TREK1 can be used to diagnose a
X X CC disease or susceptibility to a disease related to expression or activity
X X CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the
X X CC treatment of diseases including cancer, pulmonary, cardiovascular, and
X X CC inflammatory diseases, pain, psychiatric disorders including depression
X X CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
X X CC stroke, and head trauma and neurological disorders including migraine.
X X CC
X X SQ Sequence 411 AA;

Query Match 96.9%; Score 2095; DB 20; Length 411;
Best Local Similarity 95.9%; Pred. No. 3.4e-203;
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAADLDLPKSAONSKPRLSFSTRPTVLASRVESDPTTINVMKKVTSTPLVVLVLI 60
Db 1 maepdlldpkksaonskprlsfstrptvlasrvesdpttinnvmkkvtstpllvvlyli 60

systems in humans and animals, e.g. epilepsy, cardiovascular diseases (arrhythmia). neurodegeneration (particularly where associated with

DR N-PSDB; AAA27105.

DR WPI; 2000-365583/

XX	learning disorder; memory disorder; age-related memory loss; obesity;
KW	neurological disorder; cardiac disorder; gene therapy.
XX	
OS	Homo sapiens.
PN	WO200052164-A2.
XX	
PD	08-SEP-2000.
XX	
PF	01-MAR-2000; 2000WO-US05409.
XX	
PR	01-MAR-1999; 99US-0259951.
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PT	Curtis RAJ;
XX	
DR	WPI; 2000-572183/53.
DR	N-PSDB; AAA37770, AAA37771.
XX	
PT	New tandem of P domains in a weak inward rectifying potassium channel proteins and genes for e.g. developing therapeutic agents for potassium channel associated disorders, e.g. central nervous system, psychiatric disorders
PT	
XX	
PS	Disclosure; Fig 1; 148pp; English.
XX	
CC	This sequence represents the human TWIK-2 protein of the invention. The
CC	TWIK-2 (tandem of P domains in a weak inward rectifying potassium (K ⁺)
CC	channel-2), TWIK-3 and TWIK-4 nucleic acids and proteins are useful as
CC	targets for developing modulating agents to regulate a variety of
CC	cellular processes. They may be useful for developing novel diagnostic
CC	and therapeutic agents for potassium channel associated disorders,
CC	e.g. central nervous system disorders (e.g. Alzheimer's disease,
CC	dementia, Parkinson's disease, multiple sclerosis, amyotrophic lateral
CC	sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jacob
CC	disease), psychiatric disorders (e.g. depression, schizophrenia
CC	disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic
CC	disorders), learning or memory disorders (e.g. amnesia or age-related
CC	memory loss), neurological disorders (e.g. migraine), obesity, and
CC	cardiac disorders. The nucleic acids, proteins, protein homologues and
CC	antibodies against them may be further used in screening assays,
CC	and predictive medicine. The nucleic acids can be inserted into vectors and
CC	used as gene therapy vectors, to express TWIK protein, to detect TWIK
CC	mRNA, modulate TWIK activity, and screen for drugs or compounds that
CC	modulate TWIK activity. Host cells may be used to produce non-human
CC	transgenic animals.
XX	
Sequence	499 AA;
XX	

[illegible]

Db	242	vnw-----kvsnf-----vevkhaklriri-----rkcsf 267
Oy	353	ELAGHNHDELTPCRRLTSVNHLINERDV--LPLPLKTES: 391
Db	268	e-spsfs-----fkalgxvgsstaskdvnfsfkskce 301
RESULT 11		
ID	AAV79675	
AC	AAV79675	standard; Protein: 499 AA.
XX	AAV79675:	
XX	29-AUG-2000	(first entry)
XX	Human potassium channel TASK2.	
XX	TASK2: TWIK-related acid-sensitive K ⁺ chann	2; human;
XX	potassium channel; drug screening; hypertensio	
XX	hypotensive; transplant rejection; therapy; diagnosis.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	Domain	8..26
XX	Domain	/note="transmembrane domain 1"
XX	Domain	113..133
XX	Domain	/note="transmembrane domain 2"
XX	Domain	158..180
XX	Domain	/note="transmembrane domain 3"
XX	Domain	229..250
XX	Domain	/note="transmembrane domain 4"
XX	Domain	85..133
XX	Domain	/note="P domain"
XX	Domain	190..215
XX	Domain	/note="P domain"
XX	Modified-site	77
XX		/note="N-glycosylated"
XX	W0200027871-A2.	
XX	18-MAY-2000.	
XX	09-NOV-1999;	99MO-IB01986.
XX	09-NOV-1998;	98US-0107692.
XX	08-NOV-1999;	99US-0436265.
XX	(CNRS) CNRS CENT NAT RECH SCI.	
XX	Duprat F, Lesage F, Lazdunski M;	
XX	WPI: 2000-376487/32.	
XX	N-PSDB: AAA27747.	
XX	New nucleic acid encoding a non-inactivating outwardly rectifying	
XX	potassium transport channel, designated TASK2, useful in the treatment	
XX	of hypertension or dysfunctions of the kidney, liver or pancreas	
XX	Claim 16; Fig 14a; 91pp; English.	
XX	The present sequence is that of human TASK2 (TWIK-related	
XX	acid-sensitive potassium channel 2), a novel member of the 2P domain	
XX	potassium channel family that also includes TWIK-1 (see AAV79673) and	
XX	TASK1 (see AAV79674). TASK2 is a unique potassium transport channel	
XX	that is regulated by external pH, and is pre dominantly expressed in	
XX	kidney and epithelial tissues. The invention relates to:	
XX	identification of the native renal channel with the properties of	
XX	TASK2; identification of potent pharmacology that specifically	
XX	modulates the activity of the TASK-2 channel; localizing K ⁺	
XX	channels comprising the TASK2 subunit in vivo; and the generation	
XX	of mice in which the TASK2 gene has been inactivated. The invention	
XX	also relates to diagnostic tests and therapeutic methods to detect	

CC and treat human hypertension and diseases associated with kidney,
CC pancreas and/or liver dysfunctions that may arise from mutations in
CC the TAS2R gene; protect against tissue rejection in kidney, pancreas
CC and liver transplants; and identify potential drugs capable of
CC modulating TAS2R activity.

SQ Sequence 499 AA;

Query Match	20.3%	Score 427	DB 21	Length 499
Best Local Similarity	31.1%	Pred. No. 9.9e-36		
Matches 106, Conservative	60	Mismatches 121	Indels 54	Gaps 11

```

QY 54 VLVLLIIGATVAFKALDEDPHEHISQCTTIVIOKQTFISQHSQCNSTDELDLQOIVAAIINAG 113
Db 12 lfjfalgaaflevleophwreakknuytqlkhlkfeprclgqgldkilevadaagq 71
QY 114 IIPAGNINSQISHHMDLSSFFFACTVITTTGFGNISPRTEBGKTFICITIALGLPLDFGL 173
Db 72 valtgngt--fnmwnpmamfaaivtlltlygvaavakltparctfvcfyglfgypl---c 126
QY 174 LAGVGDLQSTIFGKGIAKVEDTFKMNWSQKRIIISITIFIEGCVLFVALLPAIFKHI 233
Db 127 ltwi-salqctffggrakrlqgflklrgvslkqactlctvcltllwgyvlvhlvlpfvtmvt 185
QY 234 EGRSALDLAIYVTVITLTITIGGDDYVAG-GSIEYELDPKPKPWWMLVGLATFAAVLSMI 292
Db 186 egwmyleelylsflstlctlgfdcdvagaupnsaanhalyufvelwlylglaw---lsif 241
QY 293 GDMUPLVISTKKTKEEVGEFRHAHAEMTANVALEFKETRRRLSVEIYDKFORATSIKRLISA 352
Db 242 vnm-----kvsmf-----vevnhalkkrrrr-----rkesf 267
QY 353 ELAGNHQDLPCRCRTISVNHILTERDY--LPLPLKTESIY 391
Db 268 e-sasphs-----fkalgkygstaskdvntfslfskceety 301

```

RESULT 12

ID AAY94875 standard; Protein; 499 AA.

AC AAY94875

DT 12-JUN-2000 (first entry)

Human protein clone HP10538

KM Human protein: hydrophobic domain; nutritional source; haematopoiesis;
KM cytokine production; cell proliferation; cell differentiation;
KM immune deficiency; infectious disease; autoimmune disorder; asthma;
KM multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
KM allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
KM nervous system disorder; Alzheimer's disease; Parkinson's disease;
KM Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury
KM systemic cytokine damage; tissue differentiation; contraceptive; stroke
KM coagulation disorder; myocardial infarction; inflammatory condition;
KM septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
KM nephritis; therapy.

OS Homo sapiens.

PN WO200005367-A2

PD 03-FEB-2000

PF 22-JUL-1999; 99WO-JP03929

PR 24-JUL-1998; 98JP-0208820

PR 25-AUG-1998; 98JP-0238116

PR 29-SEP-1998; 98JP-0275505

!

XX (SAGA) SAGAMI CHEM RES CENT
PA (PROT-) PROTEGENE INC.
XX
XX
PI Kato S, Kimura T;
XX
DR WPI; 2000-182694/16.

PT Novel human proteins having hydrophobic domains, useful for treating
PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
XX
PS claim 1; Page 245-247; 351pp; English.

This sequence represents a human protein of hydrophobic domains. The DNA sequences can be used as a probe or as a genetic marker. The protein can also be used as a marker, and to identify potential genetic disorders. The DNA and protein can also be used as nutritional sources or supplements. The protein exhibits cytokine, cell proliferation, cell differentiation activity, and induces production of other cytokines in certain cell populations. The protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat infectious diseases caused by viral, bacterial, fungal or other infections. The protein is also used for treating autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and conditions such as asthma, and in immune suppression after organ transplantation. The protein is useful in regulation of haematopoiesis and consequently in the treatment of myeloid and lymphoid cell deficiencies. It is also used in composite bone or tissue growth or regeneration. The protein is also used in the treatment of osteoporosis or osteoarthritis and in the treatment of periodontal disease and other tooth repair processes. The protein is used in the treatment of nervous system disorders such as Alzheimer's disease, Parkinson's disease, and Huntington's disease. They are useful for protection or regeneration and treatment of lung or liver fibrosis, repetitive injury in various tissues, and conditions resulting from systemic cytokine damage. They are also used for promoting or inhibiting tissue differentiation. They are also used as contraceptives since they exhibit activity or inhibit related activities and as a fertility inducing therapy. They are used for treating various coagulation disorders and treatment and prevention of conditions resulting from coagulation activity, e.g. myocardial infarction or stroke. They also acts as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. They are used to treat inflammatory conditions such as septic shock, sepsis, ischaemia reperfusion injury, arthritis, and nephritis. They can be used to prevent tumours.

SQ Sequence 499 AA;

Query Match	20.3%;	Score 427;	DB 1;	Length 499;
Best Local Similarity	31.1%;	Pred. No. 9.9e-14;		
Matches 106;	Conservative 60;	Mismatches 42;	Indels 54;	Gaps 11

OY	54	VVLIIIAAGVAKLEOEPHELSCOTTIVIKOPFISOH.	VNSDEDELQOUVAALNAG	113
Db	12	IIfIaIgaafleVeephmkeaknytkJhlIkelf.	gqegIdkIllevsdaagg	71
OY	114	IIPGNTSNOISHMDLSSFEFFACTVTITTCFGNISPR1	JCKRIFCIYALLGPILEGFL	173
Db	72	vAltgnqt--fmmwnpmamfaatvltitllygnvapkt	..ifcVfyglfgvpl---c	126
OY	174	LAVGGDOLGITFEKGIAKVEDFTFKMNVSOTKIRIIST.	LEGCULFPAALAIIFKHI	233
Db	127	lftw-salgrkfgyrakraqlgfltkygsvsirkagiltctv	wqvylvhlvlpfpivmtv	185
OY	234	EGWALDAIIEVVVTLTITFCGDVVA-GSDIEILDFVF	EFHMLIVGLAFVAAVLSMI	292
Db	186	egwmyiegljysfllsticstifgdgtvagvmpsanynhalz	dmwlylglaw-----IsIf	241
OY	293	GDMUVRITSKTKKEEVGEFRAHAAEWMTANVAERKETRR	LYDKFORATSIKKRLSA	352

PT channel nucleic acids and proteins, useful in assays for identifying
 PT candidate compounds which are potential pesticides or therapeutics -
 PS Claim 5; Page 87-88; 96pp; English.

CC The present sequence represents tandem pore domain weak inward potassium
 CC (K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4,
 CC TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and
 CC proteins are used in screening assays to identify candidate compounds
 CC which are potential pesticides or therapeutics. The TWIK channel nucleic
 CC acids can be used for generating mutant phenotypes in animal models or
 CC in living cells that can be used to study the ion channels, their
 CC regulation, and their use as pesticide or drug targets, and as
 CC hybridisation probes and replication/amplification primers. TWIK
 CC channel proteins are useful as immunogens to generate monoclonal or
 CC polyclonal antibodies, and in assays to identify molecules that would
 CC specifically bind to them. Genetically engineered metazoan invertebrate
 CC animals may be used in studying TWIK channel activity, and for screening
 CC and identifying new drug targets, therapeutic agents, diagnostics and
 CC prognosis useful in treating disorders associated with ion channels.

SO Sequence 361 AA:

Query Match 18.2%; Score 382; DB 22; Length 361;
 Best Local Similarity 35.2%; Pred. No. 3e-31;
 Matches 88; Conservative 51; Mismatches 89; Indels 22; Gaps 6;

QY 56 LYLIGATVFKALEOPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQIVAINAGIT 115
 DB 55 mfcsgaavfsyfeapeeralrvklgtavqkflvsnpvndadeeliveivranngvys 114
 QY 116 PLNTSNQISHWDLGSSFFPAGTIVITTTGNGNISPRTEGSKICITIALGIPLEFGLA 175
 DB 115 alenalse-pnwefgsgffastvittigtgvtbplsrngklcmfyaavgipiltvlis 173
 QY 176 GVGDQL-GTIFGKGIKAKVEDFPKMNVSQ-----TKRIITSTIIIFLFGCVLVALP 226
 DB 174 alverllipfvw-----llqvlnsklghlyqplrlrlvhlalvllvllflllp 223
 QY 227 AITFKHIE-GMSALDAIYFVITLTITGFGDYVAGSDIE-YLDFKPPVWFHILVGLAY 284
 DB 224 aaftaslepewdyldslscfistltgldyldgsahqprplykmtlctylfigltl 283
 QY 285 FAAVLSMIGD 294
 DB 284 mmlltltvfyd 293

RESULT 15
 AAM23397
 ID AAM23397 standard; Protein; 336 AA.
 XX

AC AAM23397;

XX 17-MAR-1998 (first entry)

DE TWIK-1 potassium channel protein.

XX
 KW TWIK-1 potassium channel; screening; diagnosis; transgenic animal;
 KW Tandem of P domains in a weak inward rectifying K+; antibody.

OS Homo sapiens.

XX
 PN FR2744730-A1.

XX 14-AUG-1997.

XX 08-FEB-1996; 96FR-0001565.

XX 08-FEB-1996; 96FR-0001565.

XX (CNRS) CNRS CENT NAT RECH SCI.
 PA

XX Barhanin J, Duprat F, Fink M, Guillemare M, Lazdunski M;
 PI Lesage F, Romey G;
 XX
 XX
 DR MPI: 1997-427773/40.
 N-PSDB; AAT64960.

PT Nucleic acid encoding new potassium channel designated TWIK-1 -
 PT useful for treating channel deficiency diseases, screening for
 PT active agents and for diagnosis

PS Claim 12; Figure 1b; 37pp; French.

CC The present sequence represents a protein consisting a potassium channel
 CC with the properties of a TWIK (Tandem of P domains in a weak inward
 CC rectifying K+-1 channel. This is the first member of a new family of
 CC channels consisting of 4 transmembrane segments and two P domains, and
 CC being only weakly rectifying. The cDNA, vectors, the cells expressing
 CC TWIK-1 type channels and the protein are used to compensate
 CC for deficiency of potassium channels in various tissues. Compounds
 CC for modulating activity of TWIK-1 type channels may also be useful
 CC therapeutically, e.g. for control of epilepsy, arrhythmia, vascular
 CC disease, neurodegeneration (particularly of ischemic or anoxic origin),
 CC endocrine or muscular disorders. The cDNA and the vectors can also be
 CC used to create transgenic animals (especially knock-out animals) for use
 CC as models of TWIK-1 related diseases. Analysis of the sequence of the
 CC TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies
 CC can be used to detect TWIK-1 channels and for inhibiting or activating
 CC the channels in vivo.

SO Sequence 336 AA:

Query Match 18.1%; Score 379.5; DB 22; Length 336;
 Best Local Similarity 32.5%; Pred. No. 4.9e-07;
 Matches 90; Conservative 62; Mismatches 28; Indels 17; Gaps 9;

QY 51 FLVV-VLYLIGATVFKALEOPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQIVA 108
 DB 25 flvlyllylvfsgavfsvvelpyedllrgelrkrlrlly heclseqqlqfgrvle 84
 QY 109 AINAGIIPGNTSNQISHWDLGSSFFPAGTIVITTTGNGNISPRTEGSKICITIALGIP 168
 DB 85 asnygvsvisnaagn-wnwdfalsafastvltstgynhvplsdgqkafcllysviglp 143
 QY 169 LRFELLAGYGDQUGTIFGKGIKAKVEDFPKMNVSQRIKIRISITII--FILFGCVLVALP 226
 DB 144 fclllflavavgrltvhntr--rpvlyfhlrtwgfskqvavavhavlglvtvscffli--p 199
 QY 227 AITFKHIE-GMSALDAIYFVITLTITGFGDYVAG-GSDIEYLDFFKPPVWFHILVGLAY 284
 DB 200 aavfsvleddmflsfycfistltgldyldgsahqprplykmtlctylfigltl 259
 QY 285 FAAVLSMIGDMLRVISK-----KTKEEVEGFRHAAAE 315
 DB 260 mlvyletfcfe-lhelkkfrkmfyvkkkdeqdyhllle 293

Search completed: August 28, 2001, 17:05:46
 Job time: 1891 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 16:59:11 ; Search time 36.66 Seconds
(without alignments)
854.003 Million cell updates/sec

Title: US-09-503-089a-2
Perfect score: 2100
Sequence: 1 MAAPDLDPKSAONSKPRL.....LNGLPHCAGEIAVENIK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	379.5	18.1	336	2	S65566 inward rectifier p
2	345	16.4	329	2	T43509 probable potassium
3	331.5	15.8	336	2	T32247 outward rectifier
4	319	15.2	1001	2	T13807 potassium channel
5	288	13.7	383	2	T23182 hypothetical prote
6	284.5	13.5	334	2	T19860 hypothetical prote
7	284.5	13.5	364	2	T43361 probable potassium
8	282.5	13.3	461	2	T43394 potassium channel
9	279	13.0	392	2	T25392 hypothetical prote
10	273	12.8	325	2	T45032 hypothetical prote
11	269	12.7	522	2	T15584 hypothetical prote
12	266	12.5	452	2	T24265 hypothetical prote
13	262	11.9	427	2	T21118 hypothetical prote
14	249.5	11.8	444	2	T27681 hypothetical prote
15	247	11.7	444	2	T26229 hypothetical prote
16	245.5	11.6	513	2	T30037 hypothetical prote
17	240	11.4	524	2	T28933 hypothetical prote
18	236.5	11.3	528	2	T21834 hypothetical prote
19	236.5	11.2	643	2	T26616 hypothetical prote
20	236	11.0	443	2	T21598 hypothetical prote
21	230	10.9	484	2	T43529 probable potassium
22	228.5	10.9	519	2	T16629 hypothetical prote
23	228.5	10.8	550	2	T22557 hypothetical prote
24	224	10.7	1136	2	T26953 hypothetical prote
25	218	10.4	485	2	T24201 hypothetical prote
26	217.5	10.4	335	2	S44635 f22b7.7 protein -
27	217.5	10.4	544	2	T43564 potassium channel
28	217.5	10.4	544	2	T43564 potassium channel
29	217.5	10.4	551	2	T16426 hypothetical prote

30	217.5	10.4	555	2	T43357 potassium channel
31	217.5	10.4	576	2	T43363 potassium channel
32	217.5	10.4	691	2	S46585 outward-rectifier
33	217	10.3	475	2	T27725 hypothetical prote
34	215.5	10.3	586	2	T21683 hypothetical prote
35	211	10.0	660	2	T21551 hypothetical prote
36	205.5	9.8	381	2	T43393 potassium channel
37	205.5	9.8	769	2	T27550 hypothetical prote
38	205	9.8	700	2	T23264 hypothetical prote
39	204.5	9.7	523	2	T23373 hypothetical prote
40	202.5	9.6	539	2	T23700 hypothetical prote
41	196	9.3	681	2	T19429 hypothetical prote
42	195.5	9.3	569	2	T43531 probable potassium
43	195	9.3	504	2	T22269 hypothetical prote
44	195	9.3	631	2	T26232 hypothetical prote
45	191.5	9.1	600	2	T24626 hypothetical prote

ALIGNMENTS

RESULT 1

S65566 inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #ext_change 05-Nov-1999
C:Accession: S65566

R:Lesage, F.: Guillemaire, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhan
EMBO J. 15, 1004-1011, 1996

A:Title: TWIK-1, a ubiquitously human weakly inward rectifying K(+) channel with a nove
A:Reference number: S65566; MUID:96183184

A:Accession: S65566

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-336 <LES>

A:Cross-references: EMBL:U33632; NID:g1086490; PIRN:AAB01680.1; PID:g1086491

Query Match 18.1% Score 379.5; E: 2; Length 336;
Best Local Similarity 32.5% Pred. No. 3.6e-23;

Matches 90; Conservative 62; Mismatches 28; Indels 17; Gaps 9;

QY	51	FLVV--VLYLIGATYKALEQPHISQRTTIVIOKQTFISQHSQVNSTELDLQOIVA	108
DB	25	FLVLGVLLYLVFAGVAVSSVELPEDDLRLQELRKRLRFLDEHCLSEQQLQGLAVLE	84
QY	109	AINAGTIPLCNTSNQISHMDLGSEFPAGTIVITIGGNIISPRTEGKICIIYALLGIP	168
DB	85	ASNVGVSVLSNAGSN-WNMDFTSALFPASTVLSTGYGH-VPLSDGKACCIIVSVIGIP	143
QY	169	LFQFLAGVGDDQGTIRGKIAVEDTFIKMNVSQTKIN-ESTII--FILEGCVLPVALP	226
DB	144	FTLLEFLAIVVQRIIVHTR--RPLYLFIHMGFSQVAVIVHAVLGLFVVSCEFFI--P	199
QY	227	AIFKHEH-GWSALDAIFVAVITLTIGFDYVAG-GSDIEYLDYFVAVVFWVLWGLAY	284
DB	200	AAVESVLEDDMNFLSEYFCFISLTIGLDYVGEQYNKRLRYLIGITCVLLGLIA	259
QY	285	FAAVLSMIGDMKLVISK-----KTKEVGGEFRAHAAE 316	
DB	260	MLVYLETFCE-LHELKKFRKMFYKKDKDDOVHIE 295	

RESULT 2

T43509 probable potassium channel chain n2p38 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #ext_change 21-Jan-2000

C:Accession: T43509
R:Wang, Z.W.; Salikoff, L.
submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450

A:Map position: 5
A:introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match 13.7%; Score 288; DB 2; Length 383;

Best Local Similarity 23.6%; Pred. No. 1e-15;

Matches 85; Conservative 80; Mismatches 127; Indels 68; Gaps 12;

```

OY 20 LSEFTKPTVLAHVSDPTTNNMKMT-VSTIFLVVLYLIGATVPKALEOPHEISORT 78
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 16 LRANTLPSTIRAVGCGARLRIYENARFYLICILLYLAFGLIFHMLEMEVEVDERT 75

OY 79 TI---VIQKFTISQSCVNSTELDELIOQIVAINAGIIPLGNTSNOISHWDLGSSFF 135
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 76 AIDNRMDYQKVCYKHKPLNECDPEEMVRFISGATSGLL-----NSRRFDHLSLF 129

OY 136 AGVYITIGGNISPRREGKICITIALG----IPLEFLAGVDDOCTIFGKIAT 191
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 130 SATVISTIGTSTPRPHLRFITIVGVGCTCCVLFNMLF---ERLVGTGMSYLLRS 185

OY 192 VEDTFIKMNSOTKIRIISTII-----FILFG-CVLFV 223
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 186 LRERKIRYRLAKESGNKPVITLLNEDPNESSCGGHMDNWRSPYKVFILFSMCLVLI 245

OY 224 ALPAIIFKHIEGMSALDAIYFVYITLTIGFDYVAGSDIEYL--DFYKPVVFWMLVG 281
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 246 TASAGIYSVENNNYIDSLYCFISFATIGFDYVSNQDVTMSPLDYKFNCLTLTG 305

OY 282 LAFF-----AAVLSMIGWMLRVISKTKKEVEGEFRHAHAEMTANVTAEFKERRLSV 334
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 306 ACEFYCLSNVSSIVVROLNMM--IKKMDVKV-EDRSFLC-----FKKKRRYMG 352

```

RESULT 6

hypothetical protein C40C9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19860

R:Hemby, C.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19188

A:Accession: T19860

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-334 <WIL>

A:Cross-references: EMBL:270266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1

A:Experimental source: clone C40C9

C:Genetics:

A:Gene: CESP:C40C9.1

A:Map position: X

A:introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 13.5%; Score 284.5; DB 2; Length 334;

Best Local Similarity 27.4%; Pred. No. 1.7e-15;

Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

```

OY 50 IFLVVLYLIGATVPKALEOPHEISORTIV---IOKQFIQSHSCVNSTELDELIOQI 106
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 14 LILSTFYLLFGAMVPEKLE-----SEKDTWVDEIERIDRLKHK-YNSEERLHLEFA 67

OY 107 VAINAGIIPLGNTSNOISH-WDLGSSFFAGVYITLTIGGNISPRREGKICITIAL 165
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 68 IA-----IKSLPOAGYQWOFAGAFYATVYITTVGGHSAFSTNACKLFCMIFALF 119

OY 166 GILPFLAGVDDOCTIFGKIATVEDTFIK-----MNSQTKRIIS-TIIFLFG 218
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 GVPMLGIMFOSIGBRVMTFAYSILHKFRDSLHQGFTCLQGVTPPHLWVSLTIGFVW- 177

OY 219 CVLFPALPAIFKHIEGMSALDAIYFVYITLTIGFDYV--AGSDIEYLDYKPVVWF 276
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 178 ----IVSGTMTFTIEKMSIFDAYVFCMTIFSTIGFDLPLQOVNMLQDOPLYVFATIM 233

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```

OY 277 WILGLAYFAVLAISMIGDWLRVLSKTKKEVEGEFRHAHAEMTANVTAEFKERRLSVEI 336
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 234 FILIGLAVFACVNL-----VLGFMASNADELVIA-----AQREPPSAIV 273

OY 337 YDKFORATSIKRL 350
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 274 LERFTRNSLVDSOI 287

```

RESULT 7

probable potassium channel chain n2p20 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T43361

R:Mang, Z.W.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in C. elegans.

A:Reference number: Z22450

A:Accession: T43361

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-364 <MAN>

A:Cross-references: EMBL:AF083646; PIDN:AC32857.1

Query Match 13.5%; Score 284.5; DB 2; Length 364;

Best Local Similarity 27.4%; Pred. No. 1.9e-15;

Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

```

OY 50 IFLVVLYLIGATVPKALEOPHEISORTIV---IOKQFIQSHSCVNSTELDELIOQI 106
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 14 LILSTFYLLFGAMVPEKLE-----SEKDTWVDEIERI-LKHK-YNSEERLHLEFA 67

OY 107 VAINAGIIPLGNTSNOISH-WDLGSSFFAGVYITLTIG--MISPRTEGKICITIAL 165
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 68 IA-----IKSLPOAGYQWOFAGAFYATVYITTVGGHSAFSTNACKLFCMIFALF 119

OY 166 GILPFLAGVDDOCTIFGKIATVEDTFIK-----MNSQTKRIIS-TIIFLFG 218
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 GVPMLGIMFOSIGBRVMTFAYSILHKFRDSLHQGFTCLQGVTPPHLWVSLTIGFVW- 177

OY 219 CVLFPALPAIFKHIEGMSALDAIYFVYITLTIGFDYV--AGSDIEYLDYKPVVWF 276
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 178 ----IVSGTMTFTIEKMSIFDAYVFCMTIFSTIGFDLPLQOVNMLQDOPLYVFATIM 233

OY 277 WILGLAYFAVLAISMIGDWLRVLSKTKKEVEGEFRHAHAEMTANVTAEFKERRLSVEI 336
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 234 FILIGLAVFACVNL-----VLGFMASNADELVIA-----AQREPPSAIV 273

OY 337 YDKFORATSIKRL 350
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 274 LERFTRNSLVDSOI 287

```

RESULT 8

potassium channel chain n2p18 homolog - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T43394

R:Kunkel, M.T.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in C. elegans.

A:Reference number: Z22479

A:Accession: T43394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-461 <KUN>

A:Cross-references: EMBL:AF083650; PIDN:AC32861.1

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:05:51 ; Search time 54.36 Seconds

(without alignments)
1000.319 Million cell updates/sec

Title: US-09-503-089A-2
Perfect score: 2100
Sequence: 1 MAAPDLDPKSAONSKPRL.....LNGILPMGAGEIAVENIK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2095	99.8	411	4	Q9NRT2
2	1249	59.5	538	11	Q9JIS4
3	1243	59.2	538	4	Q9H59
4	502.5	23.9	284	4	Q9H591
5	412.5	19.6	502	11	Q9JIS4
6	357.5	17.0	356	11	Q9JIS4
7	357.5	17.0	356	11	Q9JIS4
8	356.5	17.0	356	11	Q9JIS4
9	349.5	16.6	374	4	Q9NRC2
10	347.5	16.5	374	4	Q9NRC2
11	345	16.4	329	5	Q9H59
12	343	16.3	313	11	Q9H59
13	342.5	16.3	329	4	Q9H59
14	341	16.2	335	11	Q9JIS4
15	339.5	16.2	330	4	Q9H59
16	336	15.8	289	11	Q9H59
17	331.5	15.8	236	5	Q9H59
18	328.5	15.6	237	11	Q9H59
19	304.5	14.5	430	4	Q9H59

20	301	14.3	430	11	Q9H59
21	300	14.3	340	5	Q9H59
22	299.5	14.3	343	11	Q9JIS4
23	296.5	14.1	398	5	Q9H59
24	293.5	14.0	392	11	Q9H59
25	288	13.7	383	5	Q21094
26	287.5	13.7	408	4	Q9H59
27	284.5	13.5	364	5	Q9H59
28	284.5	13.5	385	5	Q9H59
29	282.5	13.5	461	5	Q9H59
30	280	13.3	405	11	Q9H59
31	279	13.3	393	5	Q9H59
32	273	13.0	392	5	Q9H59
33	273	13.0	1910	5	Q22426
34	269	12.8	325	5	Q18120
35	266	12.7	522	5	Q22042
36	262	12.5	452	5	Q93531
37	261.5	12.5	395	5	Q9V362
38	249.5	11.9	427	5	Q23386
39	247	11.8	444	5	Q45891
40	245.5	11.7	1539	5	Q19611
41	244.5	11.6	513	5	Q22940
42	243.5	11.6	270	11	Q9JIS4
43	243	11.6	389	5	Q9V362
44	240	11.4	524	5	Q21729
45	236.5	11.3	654	5	P90863

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	411 AA.
Q9NRT2	Q9NRT2			
AC	Q9NRT2			
DT	01-OCT-2000 (TREMREL. 15, Created)			
DT	01-OCT-2000 (TREMREL. 15, Last sequence update)			
DT	01-MAR-2001 (TREMREL. 16, Last annotation update)			
DE	TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.			
GN	TREK-1.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Meadows H.J., Benham C.D., Cairns W., Gloger J., Jennings C.,			
RA	Medhurst A.D., Murdoch P., Chapman C.G.,			
RT	"Cloning, localization and functional expression of the human ortholog			
RT	of the TREK-1 potassium channel."			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF171068; AAF89743.1; -			
DR	InterPro: IPR001622; -			
DR	InterPro: IPR003280; -			
DR	PRINTS: PR01333; 2PROKCHANNEL.			
KW	ionic channel			
SQ	SEQUENCE 411 AA: 45494 MW: FDE40CAB21B4<AT> CRC64:			

Query Match	99.8%; Score 2095; DB 1	Length 411;
Best local similarity	99.8%; Pred. No. 7.1e-143;	
Matches 410;	Conservative 1;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MAAPDLDPKSAONSKPRLSFTKPPVLAARVESDPT NVKKRTVSTFLVYVLLII 60
DB	1	MAAPDLDPKSAONSKPRLSFTKPPVLAARVESDPT NVKKRTVSTFLVYVLLII 60
QY	61	GATVFKALQPHETISORTTIVIOKQPTISOHSCVNSTELHEI LOQIYAANAGIIPGNT 120
DB	61	GATVFKALQPHETISORTTIVIOKQPTISOHSCVNSTELHEI LOQIYAANAGIIPGNT 120
QY	121	SNQISHWDLGSSFFACTVITITIGFGNISPRTEGKIFV L L G I P L C F L L A G V D Q 180

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DB 121 SNOISHWMDGSSFFAGTATTTTIGFNGNISPRTEGKIFCIITIALLGIPLEGFLAGVDGQ 180
    |||
DB 181 LGTIFKRGIAKAVEDTIFKKNVSOTKIRIISTIFILFGCVLFAALPAIFKHIEGSALD 240
    |||
DB 181 LGTIFKRGIAKAVEDTIFKKNVSOTKIRIISTIFILFGCVLFAALPAIFKHIEGSALD 240
    |||
OY 241 AIFVYITLTITGFDYVAGSDIEYLDFFKPYVMFMIWGLAVFAAVLSMIGDMLRVIS 300
    |||
DB 241 AIFVYITLTITGFDYVAGSDIEYLDFFKPYVMFMIWGLAVFAAVLSMIGDMLRVIS 300
    |||
OY 301 KTKKEVGEFRAHAEMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSAGLGNHNO 360
    |||
DB 301 KTKKEVGEFRAHAEMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSAGLGNHNO 360
    |||
OY 361 ELTPCRRITSVNLTNEDVLPPLLTKESTIYNGLTPHCGAGEIAYENIX 411
    |||
DB 361 ELTPCRRITSVNLTNEDVLPPLLTKESTIYNGLTPHCGAGEIAYENIX 411
    |||

```

RESULT 2

O9JIS4 PRELIMINARY: PRT: 538 AA.

```

AC 09JIS4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE POTASSIUM CHANNEL TREK-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20298807; PubMed=10747911;
RA Bang H., Kim Y., Kim D.;
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
RT family";
RT J. Biol. Chem. 275:17412-17419(2000).
DR EMBL; AF196965; AAF5132.1; -
DR InterPro; IPR000099; -
DR InterPro; IPR001622; -
DR InterPro; IPR003280; -
DR Pfam; PF02034; TWIK_channel; 1.
DR PRINTS; PR01333; 2PORECHANNEL.
SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0AAS2B97E4 CRC64;

```

Query Match 59.5%; Score 1249; DB 11; Length 538;
 Best Local Similarity 63.7%; Pred. No. 6, 2e-82;
 Matches 247; Conservative 55; Mismatches 64; Indels 22; Gaps 6;

```

OY 2 AAPDLDPKSA-AQNSKRLSFTSKPTVLASVEDT---TINWKKKTVSTIPLVVL 56
    |||
DB 23 AAPVQCPKSAATNGHPVRLSISRAFYVA-RMEGASOGGLQTVKMKTVAAIFVAVV 81
    |||
OY 57 YLIGATVFKALQEPHEISQRTIYIOKOTFISQHSVCNSTELDELQOIVAAI 116
    |||
DB 82 YLVTGGLVRALEQEPRESSOKNTIALEKAEFLRDHICVSPQELFTILOHADNAGVSP 141
    |||
OY 117 LGNTSNQISHMDLGSSFFAGTATTTTIGFNGNISPRTEGKIFCIITIALLGIPLEGFLAG 176
    |||
DB 142 VGNSSNSSHMDLGSAFFAGTATTTTIGFNGNISPRTEGKIFCIITIALLGIPLEGFLAG 201
    |||
OY 177 VGDQGTIGKGIKAVEDTIFKKNVSOTKIRIISTIFILFGCVLFAALPAIFKHIEGS 236
    |||
DB 202 ICDQGTIGKGIKAVEDTIFKKNVSOTKIRIISTIFILFGCVLFAALPAIFKHIEGS 261
    |||
OY 237 SALDAIFVYITLTITGFDYVAG-SDIEYLDFFKPYVMFMIWGLAVFAAVLSMIGD 295
    |||
DB 262 TALESTIEFYVVLITVGFDFVAGNAGINRYKWKPLVWFWLGLAVFAAVLSMIGD 321
    |||
OY 296 LRVISKTKKEVGEFRAHAEMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSAGL 355
    |||

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DB 322 LRVISKTKKEVGEFRAHAEMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSAGL 376
    |||
OY 356 GNNHQLTGPCRRITSVNLTNEDVLP 383
    |||
DB 377 -----RRRLGIDORAHSLDMLSP 394
    |||

```

RESULT 3

O9HB59 PRELIMINARY: PRT: 538 AA.

```

AC 09HB59;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE 2P DOMAIN POTASSIUM CHANNEL TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20435789; PubMed=10880510;
RA Lesage F., Terrenoire C., Romey G., Lazdunski S.;
RT "Human TREK2, a 2p domain mechano-sensitive K+ channel with multiple
RT regulations by polyunsaturated fatty acids, phospholipids and Gs,
RT G1, and Gq protein-coupled receptors.";
RT J. Biol. Chem. 275:28398-28405(2000).
DR EMBL; AF279890; AAG15191.1; -
KW Ionic channel.
SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D1473 CRC64;

```

Query Match 59.2%; Score 1243; DB 11; Length 538;
 Best Local Similarity 62.7%; Pred. No. 1, 7e-82;
 Matches 247; Conservative 54; Mismatches 64; Indels 28; Gaps 6;

```

OY 2 AAPDLDPKSA-AQNSKRLSFTSKPTVLASVEDT---TINWKKKTVSTIPLVVL 50
    |||
DB 17 AAPVQCPKSAATNGHPVRLSISRAFYVA-RHLSOGGLQTVKMKTVAAI 75
    |||
OY 51 FLVVLVYLIGATVFKALQEPHEISQRTIYIOKOTFISQHSVCNSTELDELQOIVAAI 110
    |||
DB 76 FLVVLVYLIGATVFKALQEPHEISQRTIYIOKOTFISQHSVCNSTELDELQOIVAAI 135
    |||
OY 111 LGNTSNQISHMDLGSSFFAGTATTTTIGFNGNISPRTEGKIFCIITIALLGIPLEGFLAG 170
    |||
DB 136 NGVSPDIGNSSNSSHMDLGSAFFAGTATTTTIGFNGNISPRTEGKIFCIITIALLGIPLEGFLAG 195
    |||
OY 171 GFLLAGVGOLGTFKGIKAVEDTIFKKNVSOTKIRIISTIFILFGCVLFAALPAIFKHIEGS 230
    |||
DB 196 GFLLAGVGOLGTFKGIKAVEDTIFKKNVSOTKIRIISTIFILFGCVLFAALPAIFKHIEGS 255
    |||
OY 231 KHEGMSALDAIFVYITLTITGFDYVAG-SDIEYLDFFKPYVMFMIWGLAVFAAVLSMIGD 289
    |||
DB 256 KHEGMSALDAIFVYITLTITGFDYVAGNAGINRYKWKPLVWFWLGLAVFAAVLSMIGD 315
    |||
OY 290 SWIGDLRVLSKTKKEVGEFRAHAEMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSAGL 349
    |||
DB 316 SWIGDLRVLSKTKKEVGEFRAHAEMWTANVTAEFKETRRLSVEIYDKFORATSIKRLSAGL 373
    |||
OY 350 LSAELAGNHNQELTGPCRRITSVNLTNEDVLP 383
    |||
DB 374 -SME-----RRRLGIDORAHSLDMLSP 394
    |||

```

RESULT 4

O9HB59 PRELIMINARY: PRT: 294 AA.

```

AC 09HB59;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

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```

DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE D13F1.2 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K).
GN D13F1.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136087; CAC07336.1; -.
KW Ionic channel.
SQ
SEQUENCE 294 AA; 32507 MW; FCBA3B352F1E0952 CRC64;

Query Match
Best Local Similarity 23.9%; Score 502.5; DB 4; Length 294;
Matches 97; Conservative 56; Mismatches 83; Indels 13; Gaps 5;

QY 47 VSTIFLVVLYLLIGATVFKALDQPHISQRTIYVIOKQTFISQHSVNSTELDELIOQI 106
DB 14 VLPLLLAYVCYLLLGATIPQLLRQAEASRDQFOLEKLFLENLYTCLDQMAHEQVQVI 73
QY 107 VAAINAGIPLGNTSNOISHWDLGSSFFAGVITTTIGFNGISPRTEGKIFCIYALLG 166
DB 74 MEAVMGVGNPKGNSTNP-SNMDFGSSFFAGVITTTIGYCNLAPSTEAGQVFCVFALLG 132
QY 167 IPLFGFLAGVGQDLGTIFPKGIAKVEDTFIKNNVSOTK---IRIISTIFILFGCVLFV 223
DB 133 IPLNVIFL---NHLGTGLRAHLAIE---RWEDRRRSQVQLVGLALFTLGLVIL 184
QY 224 ALPAIFKHIEGMSALDAITFVVITTTIGFGVAGASDIE-YLDFYKPVWFMIYGL 282
DB 185 IFPPMVFNSHEGMSFSEGFYFATITLTICGDIYVGTDPKSHIVYSRLAAILLGL 244
QY 283 AYFAAVLSM 291
DB 245 AWLALILPL 253

RESULT 5
QY 09J62 PRELIMINARY; PRT; 502 AA.
AC 09J62;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SVJ; TISSUE=KIDNEY;
RA Roux J.; Barhanin J.;
RT "Mouse two p domain potassium channel TASK2.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RA Cid L.P.; Niemeyer M.I.; Sepulveda F.V.;
RT "Functional properties of mouse TASK-2 potassium channel.";
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258395; AAF68668.1; -.
DR EMBL; AF319542; AAG35065.1; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR003280; -.
DR PRINTS: PRO1333; 2POREKCHANL.
KW Ionic channel.
SQ
SEQUENCE 502 AA; 55976 MW; E4C7E7CC71B44D95 CRC64;

```

```

Query Match
Best Local Similarity 19.6%; Score 412.5; DB 4; Length 502;
Matches 94; Conservative 65; Mismatches 85; Indels 35; Gaps 9;

QY 54 VVLIILIGATVFKALDQPHISQRTIYVIOKQTFISQHSVNSTELDELIOQI 113
DB 12 IIFLYLAIGAIFVELEPHKREAKKNYYTKLHLKEPP---JEGDLKILQVSDADOG 71
QY 114 IIPLGNTSNOISHWDLGSSFFAGVITTTIGFNGISPRTEGKIFCIYALLGIPFGFL 173
DB 72 VAITGNQT--FNNMNNPNAIFATVITTTIGYCNVAPKT---GLFCVFGFLFVPL---C 126
QY 174 LAGVGDLGTIFPKGIAKVEDTFIKNNVSOTKIRIISTITLFGCVLFVAPLAIIFKHI 233
DB 127 LTFVI-SALGKFFCGRAKRLQGLFLTRGVSLRKAKQITCTA---VAGVVLHVLVPEVFNMT 185
QY 234 EGSALDAITFVVITTTIGFGDVAG-GSDIEYLDYK---VWFLLVGLAIFAAVLSMI 292
DB 186 EEMNYIEGLYSPTITTTIGFGDVAGVNPANVHALYR VETWYGLAW---LSLF 241
QY 293 GDLRVYISKTKREVGEPFRAHAEMWANTAEKETRFR---VELYKFORATSIKRLSA 352
DB 242 VNM-----KVSNF-----VEVHKAIKRRRR---ESFSSPSKRAL-- 277
QY 353 ELAGN 357
DB 278 QMAGS 282

RESULT 6
QY 09Z2T2 PRELIMINARY; PRT; 336 AA.
AC 09Z2T2;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PUTATIVE POTASSIUM CHANNEL TWIK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L.; Joiner W.J.; Quinn A.M.; Wang L.-Y.; H.thes T.;
RA Kaczmarek L.K.;
RT "Cloning and localization of TWIK, a putative potassium channel with
RT two p domains.";
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022819; AAD09336.1; -.
DR InterPro: IPR000099; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR001779; -.
DR InterPro: IPR003280; -.
DR Pfam: PF02034; TWIK_channel.1.
DR PRINTS: PRO1333; 2POREKCHANL.
DR PRINTS: PRO1096; TWIK1CHANNEL.
KW Ionic channel.
SQ
SEQUENCE 336 AA; 38228 MW; 5E78031947D75 CRC64;

Query Match
Best Local Similarity 18.0%; Score 378.5; DB 4; Length 336;
Matches 90; Conservative 62; Mismatches 10; Indels 17; Gaps 9;

QY 51 FLVY--VYLIIIGATVFKALDQPHISQRTIYVIOKQTFISQHSVNSTELDELIOQI 108
DB 25 FLVGLVLYLVGAVVSSVELPEYDLRLROELKRLRRP EYECISEPOLDFOLCRVYE 84
QY 109 AINAGIPLGNTSNOISHWDLGSSFFAGVITTTIGFNGISPRTEGKIFCIYALLGIP 168
DB 85 ASNYGVSVLSNMSGN-WNMDFTSALTFASTVLTSTIGVHTVPLSDGKAFCIITYSYIGIP 143

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OY 169 LFGFLLAGVDGLGTFGKGIAKVEDTFIKMNVSOIKIRIISTII--FILFGCVLFAALP 226
 DB 144 FTLLFLTAVQGVTVAVTR--RPVLVFIHRMGSKOVAIVHAVLLGFTVSCOFFET--P 199
 OY 227 AIIFFKIE-GMSALDAIVVITLTITIGGDYVAG-GSIEIYIDFKPPVWMIIVGLAY 284
 DB 200 AAVFVLEDNMNLFESFYCFISLSTIGIGDYVPGEGYNOKRELYKIGITCYLLGLIA 259
 OY 285 FAVALSMIDMLRVISK-----KTKEVGEFRAHAAE 316
 DB 260 MLVLETFCE-LHELKFRKMFVKKDKDDOVHME 295

RESULT 7
 O9JL58 PRELIMINARY: PRT: 365 AA.
 ID O9JL58:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE POTASSIUM CHANNEL TASK3.
 GN KCN9.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxId=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN:
 RX MEDLINE=20287530; PubMed=10747866;
 RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
 RA Karschin A., Derst C.;
 RT "TASK-3, a novel tandem proe domain acid-sensitive K+ channel. An
 RT extracellular histidine as pH sensor";
 RL J. Biol. Chem. 275:16650-16657(2000).
 DR EMBL AF212827; AAF63706.1; -;
 DR InterPro: IPR000099; -;
 DR InterPro: IPR001622; -;
 DR InterPro: IPR003092; -;
 DR InterPro: IPR003280; -;
 DR Pfam: PF02034; TWIK_channel.1.
 DR PRINTS: PRO1333; 2PORECHANNEL.
 DR PRINTS: PRO1095; TASKCHANNEL.
 SQ SEQUENCE 365 AA; 40769 MW; 261DC973FF53AF91 CRC64;

Query Match 17.0%; Score 357.5; DB 11; Length 365;
 Best Local Similarity 30.1%; Pred. No. 4.4e-18;
 Matches 94; Conservative 60; Mismatches 109; Indels 49; Gaps 9;

OY 42 MKKVTSTFLV--VVLVLTIGATVFKALQEPHEISORTTIVIKQFISQHSVCNSTEL 99
 DB 1 MKKQNTSLIACCTTYLLVGAAYDALESDEHREKKAEEIRIKGKNI--STED 58
 OY 100 DELIQIVAAI--NGGIPLGNTSNOISHWDGSSFFAGTVITTTIGGNISPRTEGG 156
 DB 59 YRQLELVIIQSEPHRAGV-----QMKFAGSEFYAIVYITTTIGVGHAPGTDACK 107
 OY 157 IICIIYALGILFGLGVLGVDGLGTFGKGIAKVEDTFIKM-----NVSOIKIR 207
 DB 108 ACQMFYAVLGILPLTVMFQSLGERM-----NFEVRLIKRIKCCGMRTTEVS 155
 OY 208 IISTIFILFGCVLFAALDAIVFVITLTITIGGDYVAGSD--IE 265
 DB 156 MEMNVTGVSFGSCGTCICAAPFSCCEMSFPHAYTCITLTITIGGDYVALQSGALQ 215
 OY 266 YLDYFVPMVFMILVGLAFAAVLSMIGMLRVISKRTKEVGEFRAHAA-----EMTA 319
 DB 216 RRPVYAFSFMIVGLVTVIGAFNLV--VLRLTMNSDEEGEGEGALGONPSSVYT 273
 OY 320 NVTAEKERTRR 331
 DB 274 HISEARQVOR 285

RESULT 8
 O02821 PRELIMINARY: PRT: 259 AA.
 ID O02821:
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE DOUBLE PORE POTASSIUM CHANNEL RABCKNK1 (FRACMETH).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cricetidae.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ortas M., Velazquez R., Tung F., Desir G.V.;
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL AF004695; AAB61602.1; -;
 DR InterPro: IPR001622; -;
 DR InterPro: IPR001779; -;
 DR InterPro: IPR003280; -;
 DR PRINTS: PRO1333; 2PORECHANNEL.
 DR PRINTS: PRO1096; TWIKCHANNEL.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 259 AA; 29311 MW; 5546A8BD278E713 CRC64;

Query Match 17.0%; Score 356.5; DB 6; Length 259;
 Best Local Similarity 33.1%; Pred. No. 3.4e-18;
 Matches 78; Conservative 57; Mismatches 94; Indels 7; Gaps 5;

OY 51 FLIVV--VVLVLTIGATVFKALQEPHEISORTTIVIKQFISQHSVCNSTELDILQIYA 108
 DB 26 FLVLTGLTLVFGAVFSSVELPYEDLQELRKRPVEHECLISEQLQFGRVLYE 85
 OY 109 AINAGIIPLGNTSNOISHWDGSSFFAGTVITTTIGFNGISPRTEGGKICIIYALLGIP 168
 DB 86 ANNVCVSVASNSGN-WMNDFAFALFPAFSTVLTSTGYGCTVLSVGNKACIIIVSIVGIP 144
 OY 169 LFGFLLAGVDGLGTFGKGIAKVEDTFIKMNVSOIKIRIISTIIIFILFGCVLFAALPAI 228
 DB 145 FTLLFLTAVQGVTVAVTR--RPVLVFIHRMGSKOVAIVHAVLLGFTVSCFFIPPA 202
 OY 229 IFKHE-GMSALDAIVVITLTITIGGDYVAG-GSIEIYIDFKPPVWMIIVGL 282
 DB 203 VRSVLEDNMNLFESFYCFISLSTIGIGDYVPGEGYNOKRELYKIGITCYLLGL 258
 RESULT 9
 O9NPC2 PRELIMINARY: PRT: 374 AA.
 ID O9NPC2:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE 2P DOMAIN POTASSIUM CHANNEL TASK-3 (POTASSIUM CHANNEL TASK3) (TWO PORE
 DE POTASSIUM CHANNEL KT3.2) (2P DOMAIN POTASSIUM CHANNEL).
 GN KCN9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Girard C., Lesage F., Tinel N., Lazdunski N.;
 RT "Human Task-3, a novel 2P domain potassium channel related to Task.";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20287530; PubMed=10747866;
 RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,

RESULT	12			
09ERU5				
ID	09ERU5	PRELIMINARY;	PRT;	313 AA.
AC	09ERU5			
DT	01-MAR-2001 (TREMBLrel, 16, Created)			
DT6	01-MAR-2001 (TREMBLrel, 16, Last sequence update)			
DT7	01-MAR-2001 (TREMBLrel, 16, Last annotation update)			
DE	2P DOMAIN K+ CHANNEL TWIK-2.			
OS	Rattus norvegicus (Rat).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
OX	NCBI_TaxId=10110;			
RA	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY;			
RX	MEDLINE=20435832; PubMed=10887187;			
RA	Patel A.J., Malngret F., Magnone V., Fosset M., Lazdunski M.,			
RA	Honore E.;			
RT	"TWIK-2, an inactivating 2P domain K+ channel.";			
RL	J. Biol. Chem. 275:28722-28730(2000).			
DR	EMBL; AF281304; AAC10508.1; -.			
KW	Ionic channel.			
SO	SEQUENCE	313 AA;	34214 MW;	A93629568785CD8F CRC64;

DT 01-MAR-2001 (Tremblrel, 16, Created)
DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)
DE DJ137FL.1 (NOVEL MEMBER OF THE FORASSIUM CHANDEL SUPERFAMILY K)
DE (FRAGMENT).
GN DJ137FL.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
BL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL136087; CAC07335.1; -.
KW Ionic channel.
FT NON_TER 229
CO SEQUENCE 229 AA; 25344 MW; 7AB9FB847F242-2E; CRC64;

Qy	48	STFLVW--VLLYLIGATVFKALEOPHEISORTIVIOK	..SQHSCVNSTELDELIOQ	105
		: : : : : : : : : : : : : : : : : : : :		
Db	21	STVLLLATVLAIVLALGVTFLEEGRAAOSSRSFQDK	..ONFTCLDRPALDSLIRD	80
Qy	106	IYVAINAGITPLGNTSNQISIMWDAGSSFFPAGIYITIG	..AISPRTEGCKICITIAL	165
		: : : : : : : : : : : : : : : : : : : :		
Db	81	VVOAYKKNASLISNTTS-MGRWELVGSFVSFVSSTITIG	..SPNPMARLFCITFALV	139
Qy	166	GILPFGFLAVGOLGIFEGKGI-----AKVEDFIKMN	..VTKIRIISTIFILFCV	221
		: : : : : : : : : : : : : : : : : : : :		
Db	140	GILPLIVLV-----NRILGIMQGVVNMNASRIGF	..WQ-DPCKARMLAGSGALLSLL	191
Qy	222	FVALPAITFKHIEGMSALDAIVFVYVITLTITGFSQY	25:	
		: : : : : : : : : : : : : : : : : : : :		
Db	192	FLILPPLFLFSHMEGMSYEGEVFFILSTVGFQDY	22:	

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RESULT 14
09JULD4
ID 09JULD4 PRELIMINARY; PRT; 395 AA.
AC 09JULD4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE POTASSIUM CHANNEL TASK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Furidae; Murinae; Rattus
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=CEREBELLUM;
RX MEDLINE=20200422; Pubmed=10734076;
RA Kim Y., Bang H., Kim D.;
RT "TASK-3, a New Member of the Tandem Pore K+ Channel Family.";
RL J. Biol. Chem. 275:9340-9347(2000).
DR EMBL; AF192366; AAF60229.1;
DR InterPro; IPR000099;
DR InterPro; IPR001622;
DR InterPro; IPR003092;
DR InterPro; IPR003280;
DR Pfam; PF02034; TWIK channel; 1.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
SQ SEQUENCE 395 AA; 44365 MW; 3F76F7923A3AFCT; JRC64;

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Query Match	16.2%;	Score 341;	DB 11;	Length 395;
Best Local Similarity	30.3%;	Pred. No. 7.5e-17;		

Matches 93; Conservative 59; Mismatches 111; Indels 44; Gaps 10;

Search completed: August 28, 2001, 17:12:45
Job time: 414 sec

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OY      MKMKVSYIFLV--VVLYLIGAVFPALEOPHESORTIVIOKOFIISOHSVNSTEL    99
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1 MKROWNRJLSIACTFYTLVLGAANFALESDBHMREEULKAEEVLRCKIN-ISSDDY   59

OY      DELIQOIVA--INAGIIPLGNTSNQISHWMDGSFFPACTVITTTIGFNISPRTBGKI   157
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      60 QOLEVILOQSEPHRAGV-----QMKFASFEFATVITTYTIGYMAACDTAGRA     108

OY      FCIIYAALIDLPFGFLLAGVDOLGTTFEGKIAKVDEFTFKW-----NVSOTKIRT   208
         || :||:||||| :| :|| :| :|| :| :|| :| :|| :| :|| :| :|| :| :||
Db      109 FCMFEVAVALGIDLTVLMQSGERN-----NTFRYLILKRICKCCGRNTEFSVM    156

OY      ISTIIFIIFCGCVLFVALPAITFKHIIEGMSALDAIFYEVITLTITTGSDVYAGSD--IEY   266
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      157 ENMYTVGFSCMGCLVPW-AAAFSQCEDMSEFHAYUYCFITLTITGFDSPVALOSKCALOR   215

OY      LDFKPVRWFMLGLGVAFVAVISMIDMWLRVISKKKEEY--GEFAHAHEMTANTYTAE     324
         || | | | :| :| | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      216 KPFWAASEFMILVGTVIGAFLNV--VFRELTIMNDEDPLELGEVAQIILGNPRRYVVR   273

OY      FKETRRR    331
         ::|:|
Db      274 VPQSRR    280
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RESULT 15

ID	Q9H427	PRELIMINARY;	PRT;	330 AA.
AC	Q9H427;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	DJ781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK (KCNC3)).			
GN	DJ781B1.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lovell J.;			
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; A1118522; CAC14068.1;			
SO	SEQUENCE 330 AA; 3622 MW; 24F428721A1C7790 CRC64;			

Query Match	16.28	Score 339.5	DB 4	Length 330
Best Local Similarity	34.58	Pred. No. 7.7e-17		
Matches 90	Conservative 42	Mismatches 96	Indels 33	Gaps 9

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OY IFVLVVLITLIGAVFNKLEDPHEPHISORTTIVIOKOFISO---HSCVNSTELDEILOOI 106
   50 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 11 LVLTCLTCLLVGAVPDALESEAE-SGRÖRLIVOKRALRRKEFSMEDYRELRELLALQ- 68

OY 107 VAAINAGIIPLGNTSNOISHWDLGSSFFFGACTVITTTIGFGNISPRREGKIFCIYALIG 166
   69 AEPHRAG-----RÖKMFPGSEYFATVITTTIEYGHAAAGTDSGKVFCEMFYALIG 117

Db 167 IPLFGLLAGVGDOLGTITFGCGIAKXVEDTF-IKNNVSQTKIRIISTITITFLFGCVLFVAL 225
   118 IPLTLVTFPOSIGERLMAVNRRLTLAAKCCGLRMTCVSTE---NLVAGLLCAACATLAL 173

Db 118 IPLTLVTFPOSIGERLMAVNRRLTLAAKCCGLRMTCVSTE---NLVAGLLCAACATLAL 173

OY 226 PAIEFKHIEGSSALDAIFYVVTITTTIGFGDYGVAAGSDIEDYLFYKRPVWF---WILVGL 282
   174 GAVAFSHREGMTFFHAYVYCEITLITTTIGFGDGVALQSG-EALQRLKLPYAVFSLYITLGL 232

OY 283 AYFAAVLSMT-----GDM 295
   233 TVIGAFNLVLVLRFLVASADM 253
Db

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:05:46 ; Search time 47.95 Seconds
(without alignments)
519,634 Million cell updates/sec

Title: US-09-503-089a-4
Perfect score: 2090
Sequence: 1 MAAPDLDPKSAQNSKPRL.....LNGLPHCAGEDIAVENKK 411

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_0601:*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2084	99.7	411	20	AAV28497
2	2044	97.8	411	20	AAV34133
3	2044	97.8	411	20	AAV28496
4	2044	97.8	411	22	AA550044
5	1864	89.2	370	20	AAV30648
6	797	38.1	393	21	AAV94425
7	797	38.1	393	21	AAV94426
8	770.5	36.9	398	20	AAV30647
9	551	26.4	107	20	AAV28498
10	420	20.1	499	21	AAV90356
11	420	20.1	499	21	AAV9675

12	420	20.1	499	21	AAV94875	Human protein clon
13	392	18.8	361	22	AA831805	Amino acid sequenc
14	387	18.5	332	21	AAV90354	Human TWIK-3 prote
15	376.5	18.0	336	18	AAW23397	Human TWIK-1 potassiu
16	376.5	18.0	336	21	AAV96673	Human TWIK-1 potassiu
17	370	17.7	394	21	AAV96674	Human TWIK-1 potassiu
18	370	17.7	394	21	AAV96674	Human TWIK-1 potassiu
19	345	16.5	405	21	AAV95230	Human signal peptid
20	342.5	16.4	374	21	AAV95230	Human TWIK-1 potassiu
21	342.5	16.4	374	21	AAV95230	Human TWIK-1 potassiu
22	342	16.4	313	20	AAV34132	Human TWIK-1 potassiu
23	342	16.4	313	20	AAV34132	Human TWIK-1 potassiu
24	342	16.4	313	21	AAV90355	Human TWIK-4 prote
25	342	16.4	313	21	AAV90355	Human TWIK-4 prote
26	342	16.4	313	21	AAV90355	Human TWIK-4 prote
27	317.5	15.2	408	22	AA831804	Human TWIK-4 prote
28	299.5	14.3	395	22	AA831801	Human TWIK-4 prote
29	256.5	12.3	395	22	AA831801	Human TWIK-4 prote
30	219	10.5	336	17	AA831806	Human TWIK-4 prote
31	216.5	10.4	995	22	AA831800	Human TWIK-4 prote
32	210.5	10.1	995	22	AA831799	Human TWIK-4 prote
33	184.5	8.8	383	21	AAV96677	Human TWIK-4 prote
34	172	8.2	1153	22	AA831802	Human TWIK-4 prote
35	160.5	7.7	347	21	AAV96676	Human TWIK-4 prote
36	152.5	7.3	197	20	AAV34126	Human TWIK-4 prote
37	144.5	6.9	316	21	AAV34160	Human TWIK-4 prote
38	144.5	6.9	316	21	AAV34160	Human TWIK-4 prote
39	144.5	6.9	408	21	AAV34159	Human TWIK-4 prote
40	144.5	6.9	408	21	AAV34159	Human TWIK-4 prote
41	138.5	6.6	248	21	AAV34161	Human TWIK-4 prote
42	138.5	6.6	248	21	AAV34161	Human TWIK-4 prote
43	137.5	6.6	399	21	AAV341831	Human TWIK-4 prote
44	137.5	6.6	424	21	AAV341830	Human TWIK-4 prote
45	137.5	6.6	436	21	AAV341829	Human TWIK-4 prote

ALIGNMENTS

RESULT 1
ID AAV28497 standard; Protein: 411 AA.
AC AAV28497;
XX
XX 12-OCT-1999 (first entry)
XX
XX Mouse h-TREK1 polypeptide.
XX
XX h-TREK1; two pore potassium channel; inflammatory disease;
XX chromosome 1q32.
XX
XX Mus musculus.
XX
XX WO9937762-A1.
XX
XX 29-JUL-1999.
XX
XX 02-DEC-1998; 98WO-EP07805.
XX
XX 09-OCT-1998; 98GB-0022135.
XX
XX 27-JAN-1998; 98EP-0300570.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Chapman CG, Meadows HJ;
XX
XX WPI: 1999-469126/39.
XX
XX N-PSDB; AA200040.
XX
XX New two pore potassium channel used for, e.g. treatment of cancer,
XX pulmonary, cardiovascular and inflammatory diseases

RESULT	3
ID	AAY28496
XX	AAY28496 standard; Protein; 411 AA.
AC	
XX	AAV28496;
XX	
DT	12-OCT-1999 (first entry)
XX	
DE	h-TREK1 polypeptide.
XX	
KW	h-TREK1; two pore potassium channel; inflammatory disease;
XX	chromosome 1q32.
OS	Homo sapiens.
XX	
PN	WO9937762-A1.
XX	
PD	29-JUL-1999.
XX	
PF	02-DEC-1998; 98MO-EP07805.
XX	
PR	09-OCT-1998; 98GB-0022135.
XX	27-JAN-1998; 98EP-0300570.
PA	(SMIK) SMITHKLIN BEECHAM PLC.
PI	Chapman CG, Meadows HJ;
XX	
DR	WPI, 1999-469126/39.
N-PSDB:	AAZ00039.
PT	New two pore potassium channel used for, e.g. treatment of cancer,
XX	pulmonary, cardiovascular and inflammatory diseases
XX	
PS	Claim 3; Page 24; 44pp; English.
XX	
CC	This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1
CC	polynucleotide AAZ00039. h-TREK1 is a two pore potassium channel, and
CC	the gene maps to human chromosome 1q32, between the markers DIS217 and
CC	MIS105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
CC	disease or susceptibility to a disease related to expression or activity
CC	of h-TREK1 polypeptides. The methods of diagnosis may be used in the
CC	treatment of diseases including cancer, pulmonary, cardiovascular, and
CC	inflammatory diseases, pain, psychiatric disorders including depression
CC	and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC	stroke, and head trauma and neurological disorders including migraine.
XX	
SQ	Sequence 411 AA;
XX	
Query Match	97.8%; Score 2044; DB 20; Length 411;
Best Local Similarity	96.4%; Pred. No. 3, 1e-213;
Matches 396; Conservative	11; Mismatches 4; Indels 0; Gaps 0
OY	1 MAAPDLPPKSAOAKSPPLSSSKPTVLASRVESDASAINMKMTKVSTFLVVLYLTI 60
Db	1 maapolldpkssaaqnskprlfsctkpcvlasrvesdtlnvmkwkvstflvvlylll 60
OY	61 GAAVRALEQPOPEIORSORTTIVIOKOFIIAQHACVNSTELDELTOQTVAATNAGIIFLGNS 120
Db	61 gatlvekaieqpeisagrttlivlkqgfflsqhscvnsteidellqglvaalnaglilplgt 120
OY	121 SNOVSHMDLGSSFFFRAGTYITTTIGCNISPRREGKIFCIITVALGLPFGFLLAGVDQ 180
Db	121 snqlshwmdlgssfffragtvtlttfgnlsprteggkficfiyalldipilgfilagvgdq 180
OY	181 LGTTFGKGIAKVEDTFPIKNVSNOTKRIRISTITFIIFGCVLPALAAVAFPKRHEGSALD 240
Db	181 lgttfkgakavedtfikmvsvqtksrlitstliffgcylfalrpailifkhlegasald 240
OY	241 AIYEVVITLTJTTFGGDYVAGSDIEYLDFYKKPVVEMWILVGLAFAAVLSMIGDWLRVIS 300

Db	241	aiyfvvltlttfgfdyaggsdiedyldfipkvvfwllt	300
Qy	301	KKTKEEVEEFAHAAEWTANTTAERKTRRRSVITTD	360
Db	301	kktkeevgefahaaewtanvtaefketrirrsveiykldq	360
Qy	361	ELTPCRRLSNVHLTSEREVLPILKASIVYNGLTPLH	411
Db	361	eltpcrflsvnhltserdvpilpktesiyngltph	411
RESULT 4			
ID	AAB50044	standard; Protein: 411 AA.	
XX	AAB50044;		
AC	19-MAR-2001	(first entry)	
DT			
XX			
DE	Human TREK.		
KW	Human; TREK: 2P domain potassium channel; re-l		
KW	neuronal excitability; neurotransmitter releas		
KW	neurological disorder; sleep-related disorder;		
KW	attention deficit disorder; addiction; anxiety		
KW	Parkinson's chorea; Huntington's chorea; cereb		
XX	erectile dysfunction; alopecia.		
XX			
OS	Homo sapiens.		
XX	WO200072863-A2.		
PN			
XX	07-DEC-2000.		
PD			
XX	01-JUN-2000; 2000WO-GB02107.		
PE			
FR	01-JUN-1999; 99GB-0012733.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
XX			
PI	Hervieu GJ, Meadows HJ, Randall AD;		
DR	WPI: 2001-080422/09.		
DR	N-PSDB; AAC90412.		
XX			
PT	Use of human TREK1 polypeptide, polynucleot		
PT	modulators of h-TREK1 polypeptides for treatm		
PT	disorders, addiction and dyskinesias includin		
PT	Huntington's chorea		
XX			
PS	Claim 7; Page 29; 35pp; English.		
XX			
CC	The present sequence is human TREK1 (h-TREK1).		
CC	2P domain potassium channel family of prot		
CC	control of resting membrane potential. Modul		
CC	therefore affect neuronal excitability, the		
CC	of neurotransmitter release and activity of n		
CC	modulation therefore may be useful for the tr		
CC	neurological conditions such as epilepsy, s		
CC	cognitive dysfunction, attention deficit diso		
CC	anxiety/phobia, Parkinson's and Huntington's		
CC	incontinence, erectile dysfunction or alopec		
XX			
SO	Sequence 411 AA:		
Query Match 97.8%; Score 2044; DE: Length 411;			
Best Local Similarity 96.4%; Pred. No. 3.1e-			
Matches 396; Conservative 11; Mismatches 0; Gaps 0;			
Yy	1	MAAPDLDPKSAONSKRRLSSFPYVLASRVESDSA	60

PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel
PT family of polypeptides, useful for the diagnosis and treatment of
PT h-TRAAK related disorders; e.g. depression and schizophrenia -
XX
XX
PS Claim 3; Page 21; 35pp; English.
XX
CC Functional genomics was used to identify h-TRAAK polypeptides and
CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK
CC polypeptides have homology to the 2P domain potassium channel family of
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may
CC be used in diagnostic assays for conditions related to h-TRAAK
CC imbalance and for identifying agonists and antagonists of h-TRAAK
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also
CC be useful for treatment and prevention (e.g. as vaccines) of certain
CC diseases, such as pain, psychiatric disorders including depression and
CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke
CC and head trauma and neurological disorders including migraine and
CC epilepsy. The present sequence is human h-TRAAK protein #1.
XX
SQ Sequence 393 AA;
Query Match 38.1%; Score 797; DB 21; Length 393;
Best Local Similarity 51.1%; Pred. No. 7.5e-78;
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;
QY 42 MKMKVSTIFLVVLYLIGAAVFAKLEPOEISORTIVIKQFIFQNHCVNSTEIDE 101
Db 1 msttlllaialvallyvgalviraaleqneqagrelgevefrfiahpcvsdqelgl 60
QY 102 LIQOIIVAINGIIPLGSSNOVSH-WDLGSSFEFFACTVITIGFGNISPRTEGKIFC 159
Db 61 lkevadalgsgadepetnsstnsaswdlgsaffsgtlitllygvalrtdegrlfc 120
QY 160 IYVALGPRLEGFLLAGGDQGTIFGKIGAKVEPTFKKVNVSQKRIITITIFILEGC 219
Db 121 lfyalvgiprlfllllyagvdrfgslrhylghlealflkwhvpevlvsamfllllygc 180
QY 220 VLFVALPVRIFKHEGMSALDAIYFVVTTLTIGFGDVVAGSDIEYDFKPVVWFIL 279
Db 181 llfvlprfvcymedwsklealyfvivltltvfgdyvgaqdrpqdsapayqplvwfwll 240
QY 280 VGLAVFAVLSMIGDMLRVISKRTKEVEGFRRAHAEMTAVNTA 323
Db 241 lglayfasvltlgtlwmrvsrrtraemgyltaqaaswtgcvta 284
RESULT 7
AAV94426
ID AAV94426 standard; Protein; 393 AA.
XX
XX AAV94426;
AC
XX
DT 04-AUG-2000 (first entry)
XX
DE Human h-TRAAK polypeptide #2.
XX
KW Human: h-TRAAK: potassium channel polypeptide;
KW 2P domain potassium channel; neurodegenerative disease; stroke;
KW psychiatric disorder; neurological disorder; Gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200026253-A1.
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-GB03634.
PE
XX
XX 03-NOV-1998; 98GB-0024048.
PR 07-OCT-1999; 99GB-0023668.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PA

XX
PI Chapman CG, Duckworth DM;
XX
XX WPI: 2000-365583/31.
DR
DR N-PSDB: AAA27106.
XX
PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel
PT family of polypeptides, useful for the diagnosis and treatment of
PT h-TRAAK related disorders; e.g. depression and schizophrenia -
XX
XX
PS Claim 12; Pages 21 and 22; 35pp; English.
XX
CC Functional genomics was used to identify h-TRAAK polypeptides and
CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK
CC polypeptides have homology to the 2P domain potassium channel family of
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may
CC be used in diagnostic assays for conditions related to h-TRAAK
CC imbalance and for identifying agonists and antagonists of h-TRAAK
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also
CC be useful for treatment and prevention (e.g. as vaccines) of certain
CC diseases, such as pain, psychiatric disorders including depression and
CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke
CC and head trauma and neurological disorders including migraine and
CC epilepsy. The present sequence is human h-TRAAK protein #2.
XX
SQ Sequence 393 AA;
Query Match 38.1%; Score 797; DB 21; Length 393;
Best Local Similarity 51.1%; Pred. No. 7.5e-78;
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;
QY 42 MKMKVSTIFLVVLYLIGAAVFAKLEPOEISORTIVIKQFIFQNHCVNSTEIDE 101
Db 1 msttlllaialvallyvgalviraaleqneqagrelgevefrfiahpcvsdqelgl 60
QY 102 LIQOIIVAINGIIPLGSSNOVSH-WDLGSSFEFFACTVITIGFGNISPRTEGKIFC 159
Db 61 lkevadalgsgadepetnsstnsaswdlgsaffsgtlitllygvalrtdegrlfc 120
QY 160 IYVALGPRLEGFLLAGGDQGTIFGKIGAKVEPTFKKVNVSQKRIITITIFILEGC 219
Db 121 lfyalvgiprlfllllyagvdrfgslrhylghlealflkwhvpevlvsamfllllygc 180
QY 220 VLFVALPVRIFKHEGMSALDAIYFVVTTLTIGFGDVVAGSDIEYDFKPVVWFIL 279
Db 181 llfvlprfvcymedwsklealyfvivltltvfgdyvgaqdrpqdsapayqplvwfwll 240
QY 280 VGLAVFAVLSMIGDMLRVISKRTKEVEGFRRAHAEMTAVNTA 323
Db 241 lglayfasvltlgtlwmrvsrrtraemgyltaqaaswtgcvta 284
RESULT 8
AAV30647
ID AAV30647 standard; Protein; 398 AA.
XX
XX AAV30647;
AC
XX
DT 18-NOV-1999 (first entry)
XX
DE A mechanically sensitive potassium channel protein TRAAK.
XX
XX Mechanically sensitive potassium channel protein; TRAAK;
KW polyunsaturated fatty acid; arachidonic acid; filizole; heart disease;
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
KW muscular disease.
XX
XX Mus sp.
OS
XX
XX WO9945108-A2.
XX
XX

PD 10-SEP-1999.
 XX 23-FEB-1999; 99WO-FR00404.
 XX 05-MAR-1998; 98FR-0002725.
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX PA
 XX PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;
 XX DR MPI: 1999-551038/46.
 XX N-PSDB; AA210606.
 PT New mechanically sensitive potassium channel, used to screen for
 PT specific modulators, potential therapeutic agents for heart and nervous
 PT system disorders
 XX
 PS Claim 2; Fig 1; 40pp; French.
 CC The present sequence represents a mechanically sensitive potassium
 CC channel protein designated TRAK. The protein is activated by
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by
 CC riluzole. The protein is used to screen for specific modulators which
 CC are useful for treating or preventing diseases of the heart and nervous
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
 CC (arrhythmia), neurodegeneration (particularly where associated with
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular
 CC disease. The protein itself may be used to treat these diseases.
 CC Antibodies specific for the protein are used to detect it in tissues,
 CC also as therapeutic inhibitors or activators.
 XX
 SQ Sequence 398 AA;
 XX
 Query Match 36.9%; Score 770.5; DB 20; Length 398;
 Best Local Similarity 49.8%; Pred. No. 5.8e-75;
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;
 OY 42 MKRKTSTFLVVLVLLIGAAVFALEPOEISORTTIVIOKOTFIAHACVNSTELDE 101
 DB 1 msttllallalllylvsgalvfqaleqhegqackmhdqfdrhpcvsqskled 60
 OY 102 LIOQIVAAINAGIIP---LGNSSNOVSHMDLGSFFPAGTIVTTIGNISPRTGGKIF 158
 DB 61 fklrlvealgganpewswsnshssawmlgsaffsgflcttlygnlvtlhdagrlf 120
 OY 159 CIYALGLPLFGFLAGVDOLGTIFGKIAYEDFTIKWNYSQTKIRIRITITFIPLFG 218
 DB 121 cllfyalvlpdlfgmllagvadrfgslrrgldghaeflkwhppglvrlsavllflig 180
 OY 219 CVLEVALPAVIFKHIGMSALDAIYEVVITLTIGFDYVAGSDIEYLDYKPVVFWI 278
 DB 181 cllfvltpftfsvmeswsklealyfvtlvtlvtgfdygdgtgnsapaydplwfwl 240
 OY 279 LVCLATFAAVLSMIGDMLRYSKTKKEVGEERFAHAEMTANTYA 323
 DB 241 llglayfasvltlignwlravsrtraemgltagaaswglvtla 285
 RESULT 9
 AAAY28498
 ID AAY28498 standard; Protein; 107 AA.
 XX
 AC AAY28498;
 XX
 DT 12-OCT-1999 (first entry)
 XX
 DE Partial h-TREK1 polypeptide.
 XX
 KW Partial h-TREK1; two pore potassium channel; inflammatory disease;
 KW chromosome 1q32.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 2
 FT /note= "Encoded by ACC"
 FT Misc-difference 6
 FT /note= "Encoded by CAA"
 XX
 XX WO9337762-A1.
 XX
 XX 29-JUL-1999.
 XX
 XX 02-DEC-1998; 98WO-EP07805.
 XX
 XX 09-OCT-1998; 98GB-0022135.
 XX 27-JAN-1998; 98EP-0300570.
 XX
 XX (SMK) SMITHKLINE BEECHAM PLC.
 XX
 XX Chapman CG, Meadows HU;
 XX PI
 XX DR MPI: 1999-469126/39.
 XX N-PSDB; AA200041.
 PT New two pore potassium channel used for, e.g. treatment of cancer,
 PT pulmonary, cardiovascular and inflammatory diseases
 XX
 PS Claim 18; Page 25; 44pp; English.
 CC This sequence is a partial h-TREK1 polypeptide encoded by the h-TREK1
 CC polynucleotide AA200041. AA200039 and AAY28498 are complete h-TREK1
 CC polynucleotide and polypeptide sequences. h-TREK1 is a two pore
 CC potassium channel, and the gene maps to human chromosome 1q32, between
 CC the markers DIS237 and W15105. The polynucleotide sequence of h-TREK1 can
 CC be used to diagnose a disease or susceptibility to a disease related to
 CC expression or activity of h-TREK1 polypeptide. The methods of diagnosis
 CC may be used in the treatment of diseases including cancer, pulmonary,
 CC cardiovascular, and inflammatory diseases, psychiatric diseases
 CC including Alzheimer's, schizophrenia, neurodegenerative diseases
 CC disorders including migraine.
 XX
 SQ Sequence 107 AA;
 XX
 Query Match 26.4%; Score 551; DE 20; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.7e-71;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 119 NSSNOVSHMDLGSFFPAGTIVTTIGGNISPRTGGK 178
 DB 1 nsngysvshwdlgsffagvtlcttlygnlspstegk 178
 OY 179 DOIGTFGKIAYEDFTIKWNYSQTKIRIRITITFIPL 225
 DB 61 dqglitfgkyakvedfllkwnvsgtkiristltililcvlval 107
 RESULT 10
 AAAY90356
 ID AAY90356 standard; Protein; 499 AA.
 XX
 AC AAY90356;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Human TWIK-2 protein.
 XX
 KW Human; TWIK-3; TWIK-4; TWIK-2; central nervous system disorder; dementia;
 KW Tandem of P domains in a weak inward rectifying K⁺ channel; epilepsy;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; depression;
 KW amyotrophic lateral sclerosis; progressive supranuclear palsy; mania;
 KW Creutzfeldt-Jacob disease; psychiatric disorder; schizophrenia disorder;
 KW Korsakoff's psychosis; anxiety disorder; phobic disorder; amnesia;

CC and treat human hypertension and diseases associated with kidney,
 CC pancreas and/or liver dysfunction that may arise from mutations in
 CC the TAS2R gene; protect against tissue rejection in kidney, pancreas
 CC and liver transplants; and identify potential drugs capable of
 CC modulating TAS2R activity.

XX Sequence 499 AA:

Query Match 20.1%; Score 420; DB 21; Length 499;

Best Local Similarity 30.8%; Pred. No. 9,4e-37;

Matches 105; Conservative 62; Mismatches 120; Indels 54; Gaps 11;

QY 54 VVLYLIIAAGVAFALDEPOEISORTTIVIOKFFIAQHACVNSTEIDELIQIYVAIINAG 113
 DB 12 ifyfaigaafevleephmkeaknhytqklhlkefpelgegdikllevsdaagg 71
 QY 114 IIFLGSSNOVSHMDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIYALGLPIFGFL 173
 DB 72 valtngqt--fnmwpmamlaftatvlttlygynvapklpgrlfcvfyglfgypl---c 126
 QY 174 LAGVGDLGTFPGKIAKVEDTFIKMNVSOIKRIISTIFILFGCVLFAVLAFAVIFKH 233
 DB 127 ltwi-salgrffggrakrlgqfltkrgvslrkaqilctvltfvlwgvvlvhlvpplfvmvt 185
 QY 234 EGMSSALDAIFVYVITLTITGFGDYVAG-GSDIEYLDYKFPVFWMLVGLAFVAAVLSMI 292
 DB 186 egwnylegyltstlgtfgdvagvpsanyhalyrfvclwylglaw-----lsif 241
 QY 293 GDMLRVISKTKKEVGEFRAHAAEWMTANVTAEKRETRRLSVEIYDKFOATSVKRLSA 352
 DB 242 vnm-----kvsmtf-----vvhkalkkrrrr-----tkesf 267
 QY 353 ELAGNHNOELTPCRRLSVNHLTSREVV--LPPILKAESIV 391
 DB 268 e-ssphs-----rkalgvaygstaskvmlfslskeety 301
 RESULT 12
 ID AAY94875
 ID AAY94875 standard; Protein; 499 AA.
 XX AAY94875;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Human protein clone HP10538.
 XX
 KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;
 KW cytokine production; cell proliferation; cell differentiation;
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200005367-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-IP03929.
 XX
 PR 24-JUL-1998; 98JP-0208820.
 PR 07-AUG-1998; 98JP-0224105.
 PR 25-AUG-1998; 98JP-0238116.
 PR 09-SEP-1998; 98JP-0254736.
 PR 29-SEP-1998; 98JP-0275505.

XX (SAGA) SAGAMI CHEM RES CENT.
 PA (PROF-) PROTEGENE INC.
 XX
 PI Kato S, Kimura T;
 XX
 DR MPI; 2000-182694/16.
 XX

PT Novel human proteins having hydrophobic domains useful for treating
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
 PS Claim 1; Page 245-247; 351pp; English.

CC This sequence represents a human protein of the invention, which has
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a
 CC genetic marker. The protein can also be used as a marker, and to identify
 CC potential genetic disorders. The DNA and protein can also be used as
 CC nutritional sources or supplements. The protein exhibits cytokine, cell
 CC proliferation, cell differentiation activities, and induces production of
 CC other cytokines in certain cell populations. The protein also exhibits
 CC immune stimulating or immune suppressing activity. It can be used in the
 CC treatment of various immune deficiencies and disorders, and to treat
 CC infectious diseases caused by viral, bacterial, fungal or other
 CC infections. The protein is also used for treating autoimmune disorders
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
 CC arthritis. It is also useful in the treatment of allergic reactions and
 CC conditions such as asthma, and in immune suppression after organ
 CC transplantation. The protein is useful in regulation of hematopoiesis
 CC and consequently in the treatment of myeloid or lymphoid cell
 CC deficiencies. It is also used in compositions for tissue growth or
 CC regeneration. The protein is also used in the treatment of osteoporosis
 CC or osteoarthritis and in the treatment of periodontal disease and other
 CC tooth repair processes. The protein is used in the treatment of nervous
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and
 CC Huntington's disease. They are useful for prevention or regeneration and
 CC treatment of lung or liver fibrosis, reperfusion injury in various
 CC tissues, and conditions resulting from systemic cytokine damage. They are
 CC also used for promoting or inhibiting tissue differentiation. They are
 CC also used as contraceptives since they exhibit activity or inhibit related
 CC activities and as a fertility inducing therapeutic. They are used for
 CC treating various coagulation disorders and in treatment and prevention of
 CC conditions resulting from coagulation activity as e.g. myocardial
 CC infarction or stroke. They also acts as receptors, receptor ligands or
 CC inhibitors or agonists of receptor/ligand interactions. They are used to
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
 CC reperfusion injury, arthritis, and nephritis. They can be used to
 CC prevent tumours.
 XX
 XX Sequence 499 AA:

Query Match 20.1%; Score 420; DB 21; Length 499;
 Best Local Similarity 30.8%; Pred. No. 9,4e-37;
 Matches 105; Conservative 62; Mismatches 120; Indels 54; Gaps 11;

QY 54 VVLYLIIAAGVAFALDEPOEISORTTIVIOKFFIAQHACVNSTEIDELIQIYVAIINAG 113
 DB 12 ifyfaigaafevleephmkeaknhytqklhlkefpelgegdikllevsdaagg 71
 QY 114 IIFLGSSNOVSHMDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIYALGLPIFGFL 173
 DB 72 valtngqt--fnmwpmamlaftatvlttlygynvapklpgrlfcvfyglfgypl---c 126
 QY 174 LAGVGDLGTFPGKIAKVEDTFIKMNVSOIKRIISTIFILFGCVLFAVLAFAVIFKH 233
 DB 127 ltwi-salgrffggrakrlgqfltkrgvslrkaqilctvltfvlwgvvlvhlvpplfvmvt 185
 QY 234 EGMSSALDAIFVYVITLTITGFGDYVAG-GSDIEYLDYKFPVFWMLVGLAFVAAVLSMI 292
 DB 186 egwnylegyltstlgtfgdvagvpsanyhalyrfvclwylglaw-----lsif 241
 QY 293 GDMLRVISKTKKEVGEFRAHAAEWMTANVTAEKRETRRLSVEIYDKFOATSVKRLSA 352

Db	242	vnw-----kvsnf-----vevkhaklrrrr-----rksef	267
QY	353	ELAGNHQELTPCRRRLSVNHLTSEBKV--LPPLLAESIRY	391
		: : : : : : : : : : :	
Db	268	e-sesphs-----rkalgvkgstasdvnlfsflskkeety	301
		: : : : : : : : : : :	
RESULT	13		
AAB31805			
ID	AAB31805	standard; Protein; 361 AA.	
AC	AAB31805;		
XX			
DT	15-MAY-2001	(first entry)	
XX			
DE	Amino acid sequence of a cpb-TWIK1 polypeptide.		
XX			
KW	Tandem pore domain weak inward potassium protein; TWIK; TWIK2; TWIK3;		
KW	TWIK4; TWIK5; TWIK6; TWIK7; TWIK1; pesticide; ion channel.		
XX			
OS	Leptinotarsa decemlineata.		
XX			
FT	Key	Location/Qualifiers	
FT	Domain	46..60	
FT	Domain	/note="Transmembrane domain 1"	
FT	Domain	125..149	
FT	Domain	/note="Pore domain"	
FT	Domain	156..176	
FT	Domain	/note="Transmembrane domain 2"	
FT	Domain	204..231	
FT	Domain	/note="Transmembrane domain 3"	
FT	Domain	235..259	
FT	Domain	/note="Pore domain"	
FT	Domain	274..296	
FT	Domain	/note="Transmembrane domain 4"	
XX			
PN	WO200109301-A2.		
PD	08-FEB-2001.		
XX			
PF	27-JUL-2000; 2000MO-US20439.		
XX			
PR	28-JUL-1999; 99US-0362842.		
PA	(GENO-) GENOPTERA LLC.		
XX			
PI	Francis-Lang HL, Gillett LA, Margolis JS, Reddy BP, Winslow JW;		
PI	Luo Y, Gendreau SB, Jacobus DA, Tietjen K, Nauen R, Jeschke P;		
DR	WPI: 2001-159864/16.		
DR	N-PSDB; AAF25381.		
XX			
XX			
CC	The present sequence represents tandem pore domain weak inward potassium		
CC	(K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4,		
CC	TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and		
CC	proteins are used in screening assays to identify candidate compounds		
CC	which are potential pesticides or therapeutics. The TWIK channel nucleic		
CC	acids can be used for generating mutant phenotypes in animal models or		
CC	in living cells that can be used to study the ion channels, their		
CC	regulation, and their use as pesticide or drug targets, and as		
CC	hybridisation probes and replication/amplification primers. TWIK		
CC	channel proteins are useful as immunogens to generate monoclonal or		
CC	polyclonal antibodies, and in assays to identify molecules that would		
CC	specifically bind to them. Genetically engineered metazoan invertebrate		
CC	animals may be used in studying TWIK channel activity, and for screening		
CC	and identifying new drug targets, therapeutic agents, diagnostics and		

[illegible]

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Result No.	Score	Query Match	Length	DB	ID	Description
1	2084	99.7	411	4	US-09-236-080-2	Sequence 6, Appl
2	2044	97.8	411	4	US-09-236-080-2	Sequence 2, Appl
3	551	26.4	107	4	US-09-236-080-4	Sequence 4, Appl
4	376.5	18.0	336	3	US-08-749-816-2	Sequence 2, Appl
5	299.5	14.3	618	1	US-08-332-312-2	Sequence 2, Appl
6	219	10.5	336	1	US-08-332-312-4	Sequence 4, Appl
7	184.5	8.8	363	3	US-08-749-816-4	Sequence 4, Appl
8	160.5	7.7	347	3	US-08-749-816-3	Sequence 3, Appl
9	119	5.7	676	4	US-09-135-021-2	Sequence 2, Appl
10	106.5	5.1	581	4	US-09-135-021-80	Sequence 80, Appl
11	101.5	4.9	831	2	US-08-677-734A-11	Sequence 11, Appl
12	100.5	4.8	832	2	US-08-677-734A-12	Sequence 12, Appl
13	96.5	4.6	834	2	US-08-677-734A-9	Sequence 9, Appl
14	96.5	4.6	834	2	US-08-677-734A-10	Sequence 10, Appl
15	96	4.6	473	1	US-08-567-236-13	Sequence 13, Appl
16	96	4.6	473	1	US-08-567-236-13	Sequence 13, Appl
17	95	4.5	888	2	US-08-746-682A-13	Sequence 13, Appl
18	95	4.5	888	2	US-08-956-242-4	Sequence 4, Appl
19	94	4.5	888	3	US-09-351-215-4	Sequence 4, Appl
20	94	4.5	626	2	US-08-956-242-2	Sequence 2, Appl
21	91.5	4.4	1159	2	US-08-936-242-13	Sequence 13, Appl
22	91.5	4.4	1159	3	US-09-351-215-13	Sequence 13, Appl
23	91.5	4.4	1159	4	US-09-226-012-2	Sequence 2, Appl
24	91.5	4.4	1159	4	US-09-226-012-2	Sequence 4, Appl
25	90	4.4	606	3	US-08-620-077B-3	Sequence 3, Appl
26	90	4.3	1872	6	5386025-6	Patent No. 5386022
27	89.5	4.3	548	3	US-08-903-139B-28	Sequence 28, Appl

45	86.5	4.1	482	4	US-08-637-823B-	Sequence 32, Appl
44	87	4.2	1480	4	US-08-459-517-17	Sequence 17, Appl
43	87	4.2	1480	3	US-07-890-509-4	Sequence 4, Appl
42	87	4.2	1480	2	US-08-466-461-4	Sequence 4, Appl
41	87	4.2	1480	1	US-08-466-886-1	Sequence 17, Appl
40	87	4.2	793	4	US-08-895-590-4	Sequence 4, Appl
39	87	4.2	793	3	US-08-374-077C-4	Sequence 4, Appl
38	87	4.2	548	4	US-08-903-139B-	Sequence 25, Appl
37	87	4.2	548	3	US-08-903-139B-	Sequence 8, Appl
36	87	4.2	548	2	US-08-676-279-5	Sequence 50, Appl
35	87	4.2	483	4	US-08-637-823B-	Sequence 6, Appl
34	87.5	4.2	483	4	US-08-637-823B-	Sequence 30, Appl
33	88	4.2	550	4	US-08-637-823B-7	Sequence 4, Appl
32	88	4.2	547	3	US-08-903-139B-7	Sequence 7, Appl
31	89	4.3	682	2	US-08-436-900A-4	Sequence 4, Appl
30	89	4.3	682	2	US-09-111-757-7	Sequence 7, Appl
29	89.5	4.3	1036	3	US-08-953-823A-57	Sequence 5, Appl
28	89.5	4.3	1036	2	US-08-720-484A-5	Sequence 5, Appl
27	89.5	4.3	1036	1	US-08-953-823A-57	Sequence 5, Appl

ALIGNMENTS

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Query Match	99.78;	Score 2084;	Dh 7;	Length 411;
Best Local Similarity	99.88;	Pred. No. 2.2e-211,		
Matches 410; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Db	1	MAAPDLDPKSAQNSKRRLSESSKPYLASRVESDSA1NTHMKKKTSTIFLVVVLII	60
Qy	61	GAAVFKALEQPOEISORTTIVIOKOTFIQACHVNSDEI1OOIYAAINAGIIPLGS	120
Db	61	GAAVFKALEQPOEISORTTIVIOKOTFIQACHVNSDEI1OOIYAAINAGIIPLGS	120
Qy	121	SNQVSHMDLSSFFPAGVITTTIGFNGISPTBEGKIF1YVALLGIPLPGLLAGVDQ	180
Db	121	SNQVSHMDLSSFFPAGVITTTIGFNGISPTBEGKIF1YVALLGIPLPGLLAGVDQ	180
Qy	181	LGTFGKCIAYVEPFIKWNSQKIRIISITFIPLGCVLFVLPVIFRHHIEGMSALD	240
Db	181	LGTFGKCIAYVEPFIKWNSQKIRIISITFIPLGCVLPVLPVIFRHHIEGMSALD	240
Qy	241	AI1EYVITLTTIGFGDYAGSDIEYDFKPYVMFMJLVQ1AFPAVL5MIGMLRVIS	300
Db	241	AI1EYVITLTTIGFGDYAGSDIEYDFKPYVMFMJLVQ1AFPAVL5MIGMLRVIS	300
Qy	301	KKTKEEYGEFRAHAAMEWTANYTAJEFKETRRLSVEIYDK1ATSVKRKLSAELAGNHQ	360
Db	301	KKTKEEYGEFRAHAAMEWTANYTAJEFKETRRLSVEIYDK1ATSVKRKLSAELAGNHQ	360
Qy	361	ELTECRRLSYVNHITSEREVLPPLKKAESTYLNGLTPH1ATNDIAV1ENKK411	

[illegible]

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Oy 219 CYLEFALPAAV---IRKHIEGSAALDAIVPVVTLTITIGGDAV-----GSDIE 265
Db 185 IALFVLPFCVGHILREL-GLSSI-SLYSYVTTTIGFDIVPTTGGANQPKPEFGWFV 242
Oy 322 TAEFETRRRLS-----VEYDKFORATSV-----KRKLS- 351
Db 297 TKDVCYLRRMLNELYLKVPYTVTDIAYTLPRNSGCI-SMYRVEPAPIPSRKAFSV 356
Oy 352 -AELAG-----NNHQLTPOR-----TLVNHISD-----REVLPULK 386
Db 357 CADWGAQREAGQVHANSDDTLKIDREKTFETAETHLITPLAKVYNALATVAPPAE 416
Oy 387 AESIYLNG 394
Db 417 QEDALYG 424

RESULT 6
US-08-332-312-4
; Sequence 4; Application US/08332312
; Patent No. 5559026
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Functional Expression of Drosophila
; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 33,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-312-4

Query Match 10.5%; Score 219; DB 1; Length 336;
Best Local Similarity 26.7%; Pred. No. 7.4e-15;
Matches 60; Conservative 36; Mismatches 77; Indels 52; Gaps 6;

Oy 120 SSNOVSH-----MOLGSEFFAGAVITITIGGNISPRITSGKIFCIYALGLIPFGPL 173
Db 15 TSNEVKRNAAEETWTFPFSSSIFPAVIVYTTIGIGNVPTJNIGKRWLILFSLGIDPL---T 71
Oy 174 LAGVGDGLGITFGKIGIARVEDFTIK-----MNVSGT 204

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Db 72 LVITADLAGFSLSEHVLWLVGNVTLKLYLLSRHRRERREHCEHSHGMDHNEEK 131
QY 205 KIIITIIIFILGCVLFAVLPVIRHIGMSALDAIYFVITLTITGGDVGAGSDI 264
Db 132 RI----PAFLVLAFLVYTAFGVLSKLEPWSFSTFYSFTTMTTGVGDLMPRDGY 187
QY 265 EYLD-----YKPVWFVILVGLAYFAVLSMIG-DWLRYI 299
Db 188 MYIILYILIGKFSMKKKKFKIFLGAIITMCIDLVGQYIRKI 232

RESULT 7

US-08-749-816-4
Sequence 4, Application US/08749816
Patent No. 6013470

GENERAL INFORMATION:

APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunki, Michel
APPLICANT: Roney, Georges
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989,6351P

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-749-816-4

Query Match 8.8%; Score 184.5; DB 3; Length 383;
Best Local Similarity 24.3%; Pred. No. 3.9e-11;
Matches 84; Conservative 54; Mismatches 114; Indels 93; Gaps 15;

QY 11 SAQNSK-PLTSSSKPTVYASRVESDSAINWKKMTVTITFLVVLVYLIGAAVRALE 69
Db 4 SMENSKIKWLSTSKDKKYLTRSLNKLPLALHTGLVLSVYALGAYLFSLSE 63
QY 70 OPOEISORTIVYOKOTFFINQACVNSTEDELIOQIVAAINNG-----I 114
Db 64 HPEELAKREKAT-----REFODLKQOPMGNTGISIENSSEOSIETVTKLI 108

QY 115 IPLGNSSNQ-----VSH-----WDLGSSFPFAGTV*V*FGNISPRTGKIFCII 161
Db 109 LMEEDAHNAHAFEPFLNHEIPKDMTFSSALVFTTTT*V*YGTIFPSAATGRCLIA 168
QY 162 YALLGIPLEGGELLAGVGD---QIGTIFGKIGIAVEDTFK*---NVSQTKIRIISTII 214
Db 169 YALLGIPLEFLVTMADGKFAAQLVT-----HCDNNMA-----IPAAIF 208
QY 215 ILFGCVLFAVLPV---IFPHIGMSALDAIYFVITLTI*FGCDYVAGSDIEYIDFK 271
Db 209 V---CLLF-AVPLVGLTGSTNITVLSVPSLSTIFL*FGCDLTPDMNVITHVLF-- 262
QY 272 PVVWFVILVGLAYFAVLSMIG---DWLRVISK---K*VGE 309
Db 263 -----LAVGVILVITTLIDIVAEMIDRVHYMGRHNGKA*LAGK 301

RESULT 8

US-08-749-816-3
Sequence 3, Application US/08749816
Patent No. 6013470

GENERAL INFORMATION:

APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunki, Michel
APPLICANT: Roney, Georges
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989,6351P

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 347 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-749-816-3

Query Match 7.7%; Score 160.5; DB 3; Length 347;
Best Local Similarity 23.7%; Pred. No. 1.1e-08;
Matches 57; Conservative 53; Mismatches 88; Indels 43; Gaps 10;

QY 52 LVVVLVLIIGAAVFKALPOEISORTIVYOKOTIAC*H*VYNSLEDELIOQIYAAIN 111
Db 44 ITLVFNLIIGAGIFVLA*---TONSSSELNENSEVSK---CLHNPDIG---GKITAEMK 93

US-068-677-734A-12
Sequence 12, Application US/068677734A
Patent No. 5871919
GENERAL INFORMATION:
APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Donowitz, Mark
APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform
TITLE OF INVENTION: NHR3.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,734A
FILING DATE: 10-JUL-1996
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0043-0000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 12:

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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US-08-677-734A-12

Query Match      4.8% ; Score 100.5 ; DA      Length 832:
Best Local Similarity 19.8% ; Pred. No. 0.09% ;
Matches 74 ; Conservative 55 ; Mismatches 4 ; Indels 151 ; Gaps 19

QY 39 INVMKRVSTFLVVLVLLILGAA--VKALDQDQELZK IYIQKQTFIAQNHCVMS 96
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 43 IYTFVHHVQDPIYALVWLVASLRIYF-----HLSAKY SVVPESALL----- 87

QY 97 TELDELQIVAINAGIIPLENSSNOVSHMDLGSSEF-----AGTVI--TTIGF 145
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 88 -----IYGLVAGGIVL--ADHIASFLTPVFFFFYLIPRIYLDAGIFMPKRLF 136

QY 146 GNISPRTEGGKIFCIYALL-----GIDPLFGLLIAGVGDQGLTFGKGIAYEDTF 196
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 SNL-----GSL--LLYANVGTVMNAATGLSLYGVLSGI----- 169

QY 197 IKMNVSTQKIRIITSTIFLFGCVLFVALPA-----VIFKHIEGNSALD--- 240
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 -----MGEIKIGILD--FLIFGSLIAAADPVAVLAVFEEVHNVEVLIITFVGESLINDAV 222

QY 241 -AIEFVITLTTFGSDVAVAGSDIEVDYFKRPVWMEI-----LYGLAFPAVLSMI 292
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 IYVILYNQSFVTLG-GDKVTG-----VDCKYKGIYSFF-----GGTFLVGVV-PAELLISLV 274

```


Search completed: August 28, 2001, 17:06:22
Job time: 526 sec

Db 221 DAATVVLVNEESFVAL-----GDNVTGDCVKGIVSFFVSLG 260
QY 279 --LVGLAYFAAVISMIGD--LRVI-----299
Db 261 GTIVGVV-FAFLSLVTRFKHVRRIIEPGFVLIISYLSITSEMLSALAILTFCGICC 319
QY 300 SKRTKEVEGEFRAHAAEMWTANTVTAEEKET 328
Db 320 OKYVKANISEOSATVTVYTKMLASSAET 348

RESULT 15

US-08-597-236-13
; Sequence 13, Application US/08597236
; Patent No. 5733765
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; TITLE OF INVENTION: EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennte & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,236
; FILING DATE:
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95201669,9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A., Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-597-236-13

Query Match 4.6%; Score 96; DB 1; Length 473;

Best local Similarity 22.8%; Pred. No. 0.12;

Matches 47; Conservative 33; Mismatches 52; Indels 74; Gaps 10;

QY 43 KMKTVSTIFLVVLYLLIGAAYFKALEQPEISORTIIVOKOTFIAQHACVNSTEIDEL 102
Db 280 KSYVYSDVEHYLATFLLGTSAPFIVIKP-----I 309
QY 103 IQQIVAAINAGIPLGSSNOVSHMD-----IGSSF--FFAGTVITTTGFGNISPR 151
Db 310 VEKVV-----SSDYASSQWYVPRFMSLMLESSFSDFGNTVIA-----AKQ 350
QY 152 TEG-----GKFCITVALLGIPLEFELLAGVDLG--TIRGKIAYVEDTFIKWNS 202
Db 351 TKGVFMTSYIGTVLCVLLGVLLPIIGLDGAGLSAMLGFLTTF--LLRVKDT-QKFFVI 406
QY 203 QTKIRI-ISTIFILFCGVFLVALPA 227
Db 407 QIKWRIFISMLIVLAQHILCLFLYPS 432

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A:Accession: T43509
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-329 <MAN>
 A:Cross-references: EMBL:AF083652; PIDN:AAC32863.1

Query Match 16.4%; Score 343; DB 2; Length 329;
 Best Local Similarity 34.1%; Pred. No. 2,7e-20;

Matches 94; Conservative 53; Mismatches 95; Indels 34; Gaps 11;

QY 42 MKKRYSTIFLVV--VLYLIGAAVKALKEQPOEISORTIVIOKQFTIAQHCVNSTEL 99
 1 MKQNRITSLIYCTLTLYLVGAADFALTEENELIQRKLVORREKLKRYMNSNA-DY 59
 DB 100 DELIQIVAAI--NAGIIPLGNSNOVSHMDLSSSFFACTVTTTGFGNISRTREGKI 157
 60 EILEEATIVASVPRKAGY-----QMKFSGAFYFATVTTTIGYGHSTPMTAGKV 108
 QY 158 FCIITVALGIPFLGFLAGVDGLTIFGKIAKVEDTFIKMNVSOIKIRIITIFILF 217
 109 FCLMVALAGIPGLIMFQSIGERMNTFAAKL-----RFRRAAGKQPIVTSDDLIFCT 163
 DB 218 GC-VLFVALPAVIFKHIEGMSALDAIEFVYITLTIGFGDYA---GGS---DIEYDEY 270
 164 GMGGLIFGCAFMSSEYEMNTYFDAYVYCFVTLTTIGFGDYALOKRGLQTPREVY-FF 222
 QY 271 KPVVFMILVGLVFAVLSMIGDMLRVISKTKREE 306
 DB 223 SLV---FILEGLTVISAANML--VLRFLMTDE 253

RESULT 3

T32347
 Outdated rectifier potassium channel homolog tkw-23 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 28-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32347
 R:Murphy, J.; Wohldmann, P.; O'Neal, D.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of C. elegans cosmid F34D6.
 A:Reference number: Z21153

A:Accession: T32347
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-336 <MUR>
 A:Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
 A:Experimental source: strain Bristol NZ; clone F34D6
 C:Genetics:
 A:Gene: tkw-23; CESP:F34D6.3
 A:Map position: 2
 A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match 15.8%; Score 329.5; DB 2; Length 336;
 Best Local Similarity 33.2%; Pred. No. 3.4e-19;
 Matches 94; Conservative 53; Mismatches 95; Indels 41; Gaps 12;

QY 42 MKKRYSTIFLVV--VLYLIGAAVKALKEQPOEISORTIVIOKQFTIAQHCVNSTEL 92
 1 MKQNRITSLIYCTLTLYLVGAADFALTEENELIQRKLVORREKLKRYMNSNA-DY 60
 DB 93 CVNSTEDELQIVAAI--NAGIIPLGNSNOVSHMDLSSSFFACTVTTTGFGNISRTREGKI 150
 61 MSNA-DYEILEEATIVASVPRKAGY-----QMKFSGAFYFATVTTTIGYGHSTP 108
 QY 151 RTGKGATICTIYALGIPFLGFLAGVDGLTIFGKIAKVEDTFIKMNVSOIKIRIITIFILF 210
 109 MTDAGVVFCLVALAGIPGLIMFQSIGERMNTFAAKL-----RFRRAAGKQPIVTSDDLIFCT 163
 QY 211 TITFIFGCVLFVALPAVIFKHIEGMSALDAIEFVYITLTIGFGDYA---GGS---D 263
 DB 164 DLITFTGMGLIFGCAFMSSEYEMNTYFDAYVYCFVTLTTIGFGDYALOKRGLQTPREVY 223

QY 264 IEYLDFFKPVVFMILVGLVFAVLSMIGDMLRVISKTKREE 306
 DB 224 PEYV-FFSLV---FILEGLTVISAANML--VLRFLMTDE 260

RESULT 4

T13807
 potassium channel protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C:Accession: T13807
 R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; et al.; M.H.
 Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
 A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from D.
 A:Reference number: Z17770; MIMD:97075152

A:Accession: T13807
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1001 <GOL>
 A:Cross-references: EMBL:U55321; NID:g3808067; P:U55321; PIDN:AAC69250.1
 C:Genetics:
 A:Gene: ORK1
 A:Cross-references: FlyBase:FBgn0017561
 A:Map position: 1

Query Match 15.6%; Score 325; DB 2; Length 1001;
 Best Local Similarity 28.8%; Pred. No. 2.9e-19;

Matches 90; Conservative 62; Mismatches 95; Indels 36; Gaps 10;

QY 50 IFLVVLYLIGAAVKALKEQPOEISORTIVIOKQFTIAQHCVNSTELDELQ 105
 DB 9 LIFVYISYLMFGAIIYHIEHGEKISRQAKQIAIA-----FELGDKNTTIOBELR 68
 QY 106 IYAINAGIIPLGNSNOVSHMDLSSSFFACTVTTTGFGNISRTREGKIICITIAL 165
 DB 69 ISDYCDKRPVTLPTDYDTPTWTFYHAFFAFVFCSTV-----SPRTFAGRMIMIAVSI 128
 QY 166 GIDPLFGLAGVDGLTIFGKIAKVEDTFIKMNVSOIKIRIITIFILF 218
 DB 129 GIVNGLIRAG-----LGEFGRFTEAIIYRRYKRYKKNST-----VLPOLGLITIVALLIG 184
 QY 219 CVLVALPAVIFKHIEGMSALDAIEFVYITLTIGFGDYA---GGSDEYLD 268
 DB 185 IAFLLPLPSWVFYFENMPSISLYSVTTTIGGDI-----GANGPKFEGGFVYQI 244
 QY 269 FKRPVFMILVGLVFAVLSMIGDMLRVISKTKREE 324
 DB 245 FV--IYWF--IFSLGYLVIMIMETITRGLQ--SKRLAVY-----SSNLKATONRIMSGVTKD 298
 QY 325 FKETRRRLSVEIV 337
 DB 299 VGILRRMLN-ELV 310

RESULT 5

T23182
 hypothetical protein K01D12.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23182
 R:Dobson, R.
 submitted to the EMBL Data Library, June 1996

A:Accession: T23182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-383 <MIL>
 A:Cross-references: EMBL:Z75543; PIDN:CAA99871.1; J:PLN:GN00023; CESP:K01D12.4
 A:Experimental source: clone K01D12
 C:Genetics:
 A:Gene: CESP:K01D12.4

Db 206 SKRELKQSDHLLREIAEVSPLYDLVLAAGLFWFAIGSAVPIPMNOLTYFDSVYFS 265
 QY 246 VITLTITGFDYVAGSDIEYLDPEYKPVWFWILVGLAYFAAVLSMIGDMLRV 299
 Db 266 YMSITITGLDIYP-----RRMDFLEPTL-IYITIGIMLTALVEQLADYFRIV 313

RESULT 14

T30037

hypothetical protein F20A1.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T30037

R:Galtung, S.; Wu, X.

A:Submitted to the EMBL Data Library, March 1996

A:Description: The sequence of C. elegans cosmid F20A1.

A:Reference number: Z20726

A:Accession: T30037

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1539 <GAT>

A:Cross-references: EMBL:U053150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F20A1.7

A:Experimental source: strain Bristol N2; clone F20A1

C:Genetics:

A:Gene: CESP:F20A1.7

A:Map position: 5

A:Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110

Query Match 12.1%; Score 252.5; DB 2; Length 1539;
 Best Local Similarity 22.3%; Pred. No. 3.6e-12;

Matches 96; Conservative 72; Mismatches 131; Indels 131; Gaps 16;

QY 25 KPTVLA SRVSDSAIN--VMKW-----KTVSTFLVNV--LYLIGAAVEKALE 69
 Db 52 RPSLSVAASIR-ESNISKRRLKYCFCTPPIKRLSTFKLLITIGLVSFGAHEFWYLE 110
 QY 70 QPOEISQRTTIVIOKQFFIAQHACVNSTELDELIOQIVAAINAGIIPLGSSNOVSHW-- 127
 Db 111 VPTDLERREGEFQHRK-----IAREVMVNLRAIYDNRREDREERMKH 153
 QY 128 -----DLG-----SSPEFAGVTITIGFGNISPTREGKIFECIIYALLGI 167
 Db 154 AILKFEDIDLEPVEIETVWTFFMSSFLYAGTIFETIGYINACKTRAGQATATVYAFVGI 213
 QY 168 PLF-----GFLA-----GVGQ-----LGIIRGKI-----AKVEDTFI 197
 Db 214 PIMLVMLTSLNNFLKWKIKITNGVSDMTLYIGVRLGITVIRODEVOKRLRYTKLAKTMK 273
 QY 198 KMNVSQ-----TKRIIST-----IIFILGCVLFAVLPVAVIF 230
 Db 274 RMLLSKRGASSTAIASNSENRNLSTPEDEDEEIEIHODPPVLTSLATVAMILLSAAYF 333
 QY 231 KHTBGSALDAIFVVTITLTIGBGDYVAGSDIEYLDPEYKPVWFWILVGLAYFAAVLS 290
 Db 334 CLPEDMTFETSFYFCISLTITIGIGDVTTPANPE-----YMIATFGVIVGLSMITVICID 387
 QY 291 MIGD-----MLRYSKTKTEVEVGEFRHAHAEMWTANVTAEFKETRRLR-----SVEIY 337
 Db 388 VLDKELAQMTALLOKLLITLEYMEAVKSGDPNAASAMMAGFGGRAKFLMPLISKNEGAKVM 447
 QY 338 DKFORATSVK 347
 Db 448 DKFKQDOSKR 457

RESULT 15

T26229

hypothetical protein W06D12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26229

R:Basnam, V.

submitted to the EMBL Data Library, November 1996
 A:Reference number: Z20177

A:Accession: T26229

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-444 <MIL>

A:Cross-references: EMBL:Z82073; PIDN:CAB04923.1; n:DB:GN00023; CESP:W06D12.2

A:Experimental source: clone W06D12

C:Genetics:

A:Gene: CESP:W06D12.2

A:Map position: 5

A:Introns: 70/3; 127/1; 170/1; 197/3; 326/1; 405/1

Query Match 11.8%; Score 247; DB 2; Length 444;
 Best Local Similarity 20.3%; Pred. No. 2.3e-11;

Matches 79; Conservative 76; Mismatches 79; Indels 108; Gaps 11;

QY 53 VVVVYLIIIGAAYF-----KALEQPOEISQRTTIVLC-----AOHACV 94
 Db 23 VLIYVSFLGGLFVLCBAENEKSLKHDNMRVLRISIAKQVFGRLQNNYSGNGSSSEF 82
 QY 95 NSTELDELIOQIVAAINAGIIPLGSSNOVSHWDLSSFFACTVITTTIGFGNISPTREG 154
 Db 83 SETKLRVRVSEYDAAMGISI-----DSKMTKTRMDINGGLVNGTIYTTTIGYGLAAETIW 137
 QY 155 GKIFCIYALLGIPRLGFLAGVGDQGTI---FGKIAKAVITFIKMNVSQTKIR---- 207
 Db 138 GRICTMLYAMIGIPIVINIINDGNMLFVDFHWONIGKQIQSILRQKRRKVSLEE 197
 QY 208 -----IISTIIFFTCVLFVALPAVIFKHIEGW 236
 Db 198 GSDIKTPIMETSSTPPSPQPNCTRPILPLVLIYLFGLKGVAV-----FAYFENW 250
 QY 237 SALDAIFEVVITLTIGFGDY-----VAGSDIEYLDPEYKPVWFWILVGLAYFAAVLSM 291
 Db 251 TLFEVSFFPISMTTIGFGFPTSHTVAVAGIV-----FILGLSVSMCINW 298
 QY 292 IGDMLVYSKTKTEV-GEFRHAHAEMWTANVTAE-----FKETRRLS 333
 Db 299 IOMOLEFIFNOIVORLENDKN-----TLSVAAESKRLVSEFGSIDPSKKTKTRRD 353
 QY 334 VEIYDKFORATSVKRLSALAGNHOEL 362
 Db 354 GNVAKYSENMENGNKLLMRFMSNHQKKM 382

Search completed: August 28, 2001, 17:07:05
 Job time: 474 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:13:13 ; Search time 21.03 Seconds

(without alignments)
669.472 Million cell updates/sec

Title: US-09-503-089a-4

Perfect score: 2090
Sequence: 1 MAAPDLDPKSAQNSKPKRL.....LNGLPHCAGEDIAVENMK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	100.0	411	CIW2_MOUSE	P97478 mus musculu
2	2011	96.2	426	CIW2_HUMAN	O95069 homo sapien
3	797	38.1	393	CIW4_HUMAN	O9ny88 homo sapien
4	770.5	36.9	398	CIW4_MOUSE	O88454 mus musculu
5	420	20.1	499	CIW5_HUMAN	O95279 homo sapien
6	376.5	18.0	336	CIW1_HUMAN	O00160 homo sapien
7	370	17.7	336	CIW1_MOUSE	O08581 mus musculu
8	370	17.7	394	CIW3_HUMAN	O14649 homo sapien
9	351	16.8	409	CIW3_MOUSE	O35111 mus musculu
10	342	16.4	411	CIW6_HUMAN	O54912 rattus norv
11	342	16.4	313	CIW6_MOUSE	O9y257 homo sapien
12	325	15.6	1001	ORX1_DROME	O94526 drosophila
13	305.5	14.6	307	CIW7_MOUSE	O9y251 mus musculu
14	300.5	14.4	307	CIW7_HUMAN	O9y242 homo sapien
15	217	10.4	691	TKR1_YEAST	P40310 saccharomyc
16	215.5	10.3	335	TKR8_CAEEL	P44410 caenorhabdi
17	122	5.8	238	YWS1_CAEEL	O10937 caenorhabdi
18	121	5.8	604	CI01_MOUSE	P97414 mus musculu
19	119	5.7	676	CI01_HUMAN	P51787 homo sapien
20	107.5	5.1	434	YIFR_SALTY	P37456 salmonella
21	106.5	5.1	334	PIT_RHIME	O30459 rhizobium m
22	105	5.0	872	ATCL_MYCPN	P78036 mycoplasma
23	103.5	5.0	649	OOX1_BACSU	P34956 bacillus su
24	102.5	4.9	839	NAH3_DIDMA	O28362 didelphis m
25	102	4.9	451	YVS3_RHIME	O33653 rhizobium m
26	101.5	4.9	831	NAH3_RAT	P26433 rattus norv
27	101	4.8	412	O85D_DROME	O9vhq2 drosophila
28	100.5	4.8	342	COBD_SYNY3	P74475 synecocyst
29	100.5	4.8	362	SSRS_MOUSE	O08958 mus musculu
30	100.5	4.8	832	NAH3_RABIT	P26442 oryctolagus
31	100	4.8	337	COX1_RHEAM	O03546 thea americ
32	100	4.8	402	Y718_METJA	O58138 methanococc
33	100	4.8	533	WVIN_SYNY3	O55179 synecocyst

RESULT	ALIGNMENTS
1	
CIW2_MOUSE	
ID	CIW2_MOUSE STANDARD; PRT; 411 AA
AC	P97438;
DT	01-OCT-2000 (Rel. 40, Created)
DT	01-OCT-2000 (Rel. 40, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTW. RECTIFYING POTASSIUM CHANNEL, PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL, TPCK1) (TREK-1 K+ CHANNEL SUBUNIT).
DE	CHANNEL SUBUNIT.
GN	KCNK2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RC	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC	TISSUE=Brain;
RA	MEDLINE=97157476; PubMed=9003761;
RA	Pink M., Duprat F., Lesage F., Reyes R., Romey J., Heurteaux C.,
RA	Lazdunski M.;
RT	Cloning, functional expression and brain localization of a novel
RT	unconventional outward rectifier K+ channel.
RL	EMBO J. 15:6854-6862(1996).
RN	[2]
RP	REVIEWS.
RC	TISSUE=Brain;
RA	Pink M., Duprat F., Lesage F., Reyes R., Romey J., Heurteaux C.,
RA	Lazdunski M.;
RT	Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RA	MEDLINE=99254548; PubMed=10321245;
RA	Patel A.J., Honore E., Lesage F., Pink M., Romey G., Lazdunski M.;
RT	Inhalational anesthetics activate two-pore K+ channel background K+ channels.
RL	Neurosci. 2:422-426(1999).
CC	- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC	- SUBUNIT: HOMODIMER (POTENTIAL).
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC	- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC	DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC	LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC	HIPPOCAMPUS AND CEREBELLUM.
CC	- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC	ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC	ISOFLURANE.
CC	- SIMILARITY: BELONGS TO THE TWO PORE DOM. FAMILY OF POTASSIUM
CC	CHANNELS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is published through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)

or send an email to license@sb-slb.ch.

CC EMBL: U73488; AAC53005.2; -
 CC MGD: MG1:109366; Kcnk2.
 DR InterPro: IPR000099; -
 DR InterPro: IPR001622; -
 DR InterPro: IPR003280; -
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.

FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 47 67 POTENTIAL.
 FT TRANSSEM 129 155 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 157 177 POTENTIAL.
 FT TRANSSEM 178 207 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 208 228 POTENTIAL.
 FT TRANSSEM 238 268 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 273 293 POTENTIAL.
 FT TRANSSEM 294 411 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY.

FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 411 AA; 45297 MW; 8f976DDD103EFA05 CRC64;

Query Match 100.0%; Score 2090; DB 1; Length 411;
 Best Local Similarity 100.0%; Pred. No. 6,4e-136;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRYESDAINVMKMKVSTFLVVLXLI 60
 DB 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRYESDAINVMKMKVSTFLVVLXLI 60

QY 61 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIOQIVAAINAGIPLGNS 120
 DB 61 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIOQIVAAINAGIPLGNS 120

QY 121 SNOVSHMDLGSFFPAGTIVTTIGFGNISPRTEGKIFCTIVALLGIPLEGFLAGDQ 180
 DB 121 SNOVSHMDLGSFFPAGTIVTTIGFGNISPRTEGKIFCTIVALLGIPLEGFLAGDQ 180

QY 181 LGTIFGKIAKVEDTFIKMNSQTKIRIISTIFILEGCVLFALPAVIRKHNIEGMSALD 240
 DB 181 LGTIFGKIAKVEDTFIKMNSQTKIRIISTIFILEGCVLFALPAVIRKHNIEGMSALD 240

QY 241 AIFPVVITLTITGFGDYVAGSDIEYLDYFKPVVWEMILVGLAVFAVLSMIGDWLRVIS 300
 DB 241 AIFPVVITLTITGFGDYVAGSDIEYLDYFKPVVWEMILVGLAVFAVLSMIGDWLRVIS 300

QY 301 KTKKEVEGEFRAHAAEHTAVTAPEKTRRLSEVEYIDKORATSVKRRKSAELAGHNQ 360
 DB 301 KTKKEVEGEFRAHAAEHTAVTAPEKTRRLSEVEYIDKORATSVKRRKSAELAGHNQ 360

QY 361 ELTPCRRTLSVNHLSREVLPLPLKAESIYINGLTPHCAGEDIAVENK 411
 DB 361 ELTPCRRTLSVNHLSREVLPLPLKAESIYINGLTPHCAGEDIAVENK 411

RESULT 2
 C1W2_HUMAN STANDARD; PRT; 426 AA.
 ID C1W2_HUMAN
 AC 095069; O9UNE3;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TRPC1) (TREK-1 K+ CHANNEL SUBUNIT).
 GN KCNK2 OR TREK.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99254548; PubMed=10321245;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romo G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";
 RL Nat. Neurosci. 2:422-426(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Price L.A., Hellings S.E., Hayashi J.H., Paul J.M.H.;
 RL Submitted (May-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GASES AND ANESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFLURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
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CC EMBL: AF129399; AAD47569.1; -
 CC EMBL: AF004711; AAD01203.1; -
 CC MIM: 603219; -
 DR DR InterPro: IPR000099; -
 DR DR InterPro: IPR001622; -
 DR DR InterPro: IPR003280; -
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.

FT DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 62 82 POTENTIAL.
 FT TRANSSEM 144 170 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 172 192 POTENTIAL.
 FT TRANSSEM 193 223 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 224 244 POTENTIAL.
 FT TRANSSEM 253 283 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 288 308 POTENTIAL.
 FT TRANSSEM 309 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
 FT TRANSSEM 378 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY SIMILARITY).
 FT TRANSSEM 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 MISSING (IN REF. 2).
 FT CONFLICT 2 16 MISSING (IN REF. 2).
 FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).
 FT CONFLICT 391 391 S -> N (IN REF. 2).
 FT CONFLICT 411 411 A -> T (IN REF. 2).
 SQ SEQUENCE 426 AA; 47016 MW; 2ABA2335D400; 7PC64;

Query Match 96.2%; Score 2011; DB 1; Length 426;
 Best Local Similarity 95.1%; Pred. No. 1.7e-14;
 Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRYESDAINVMKMKVSTFLVVLXLI 60
 DB 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRYESDAINVMKMKVSTFLVVLXLI 60

QY 16 VAAFDLDPKSAQNSKPRLSFSSKPTVLASRYESDAINVMKMKVSTFLVVLXLI 75
 DB 16 VAAFDLDPKSAQNSKPRLSFSSKPTVLASRYESDAINVMKMKVSTFLVVLXLI 75

QY 61 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIOQIVAAINAGIPLGNS 120
 DB 61 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIOQIVAAINAGIPLGNS 120

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Db 76 GATYFALEDPHEISQRTTYIKQOTFISQHSVCNSTELDELIOIYAALNAGIIPLGNT 135
QY 121 SNOVSHMDLSSFFPACTVITTTIGFNGINSPTEGKIFCIITALLGIPLEFLLAGVDQ 180
Db 136 SNOVSHMDLSSFFPACTVITTTIGFNGINSPTEGKIFCIITALLGIPLEFLLAGVDQ 195
QY 181 LGTIFGKIAKVEPTFKMNSVQTKIRIISTITITLFGCVLPAVPAVIEKHIGMSALD 240
Db 196 LGTIFGKIAKVEPTFKMNSVQTKIRIISTITITLFGCVLPAVPAVIEKHIGMSALD 255
QY 241 AIYVVVTLTTIGFGDVAGGSDEIYDFYKPYVFWMLVGLAFAVLAISGMGLAVIS 300
Db 256 AIYVVVTLTTIGFGDVAGGSDEIYDFYKPYVFWMLVGLAFAVLAISGMGLAVIS 315
QY 301 KTKEEVGEFRAHAEMTANTVAEFKTRRLSVEYIDKFORATSVKRLSAEAGAHNQ 360
Db 316 KTKEEVGEFRAHAEMTANTVAEFKTRRLSVEYIDKFORATSVKRLSAEAGAHNQ 375
QY 361 ELTPCRRTLSVNLTSREVLPLLKAESYVNLGLTPHCGEDIAVIENMK 411
Db 376 ELTPCRRTLSVNLTSREVLPLLKAESYVNLGLTPHCGEDIAVIENMK 426

RESULT 3
C1M4_HUMAN STANDARD; PRT; 393 AA.
AC GNGY8;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-
DE STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX PubMed-11042359;
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA Kestell R.E., Muddock P.R., Randall A.D., Rennie G.I., Glover I.S.;
RT "Cloning, localisation and functional expression of a novel human,
RT cerebellum specific, two pore domain potassium channel.";
RL Brain Res. Mol. Brain Res. 82:74-83(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Frontal cortex;
RA Gray A.T.;
RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RT chromosome 11.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC -----
CC EMBL: AF248242; AAC31731.1;
CC DR EMBL: AF247042; AAF64062.1; ALT_INIT.
CC DR InterPro: IPR001622;
CC DR InterPro: IPR003280;

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DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 3
FT TRANSMEM 4 24 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 113 POTENTIAL.
FT TRANSMEM 118 138 PORE-FORMING (POTENTIAL).
FT TRANSMEM 140 171 POTENTIAL.
FT TRANSMEM 172 192 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 221 POTENTIAL.
FT TRANSMEM 234 254 PORE-FORMING (POTENTIAL).
FT TRANSMEM 255 393 POTENTIAL.
FT CARBOHYD 78 78 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 82 82 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 328 328 P -> L (IN REF. 2).
SQ SEQUENCE 393 AA; 42704 MW; 7E1B53A0A9AL57D CRC64;

Query Match 38.1%; Score 797; DB 1; Length 393;
Best Local Similarity 51.1%; Pred. No. 1.2e-4;
Matches 145; Conservative 60; Mismatches 27; Indels 2; Gaps 1;

QY 42 MKKTVSTIFLVVLYLITIGANVKALEPOEISQRTTYIKQOTFIAQACVNSTELDE 101
Db 1 MRSTTLALALVLYLVSGALYFRALEOPHEQAOQREL...DEKFLRAHPCHVDDELGL 60
QY 102 LIOOIVAINAGIIPLGNSNOVSH--WDGSSFFPACTV...IGFNGISPRTEGKIFPC 159
Db 61 LIKEVADALGGADPEPNSNSNSHSAWDGSAFFSGTT...TLGCVNVAKRTDAGRLFC 120
QY 160 IYVALGIPLEFGLAGVGDLGTFIFGKIAKVEDPTFK...SOTKRIIISTITITLFGC 219
Db 121 IFVALVGIPLFGLIAGVGRGLSSLRHNGIHEAIFLN...VELRVLSAMFLILGIC 180
QY 220 VLFVALPAVIFKTHGESSALDAITFVYITLTTIGFGYVAGSDEIYDFYKPYVFWML 279
Db 181 LFLVLPFPFVFCVMEWSKEAIFVITVLTTFVGFYVAGADRDOSPAPVPLWEMIL 240
QY 280 VGLAYFAVLSMIGDMLRVISKTKKEEVEFRAHAEMTANTVA 323
Db 241 LGLAYFAVSLTTIGNMLRVVSRRTRAEMGILTAQAASTGIVTA 284

RESULT 4
C1M4_MOUSE STANDARD; PRT; 398 AA.
AC 088454;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-
DE STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Rodidae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MBDLINE-98292450; PubMed-9628867;
RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA Lazdunski M.;
RT "A neuronal two p domain K+ channel stimulus J by arachidonic acid and
RT polyunsaturated fatty acids.";
RL EMBO J. 17:3297-3308(1998).
RN [2]
RP ACTIVATION.
RX MBDLINE-99254548; PubMed-10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Mery G., Lazdunski M.;
RT "Inhalational anesthetics activate two pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).

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CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
 CC EXTERNAL K+ CONCENTRATIONS.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
 CC 2/TRAAT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
 CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
 CC TESTIS.
 CC -1- MISCELLANEOUS: ACTIVATED BY ARCHIDONIC ACID AND OTHER UNSATURATED
 CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
 CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLOURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF056492; AAC40181.1; -.
 CC DR MGD: MGI:1298234; KCMK4.
 CC DR InterPro: IPR000099; -.
 CC DR InterPro: IPR001622; -.
 CC DR InterPro: IPR003280; -.
 CC DR Pfam: PF02034; TWIK_Channel; 1.
 CC DR PRINTS: PRO1333; 2PORECHANNEL.
 CC DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 CC Glycoprotein; Alternative splicing.
 CC FT DOMAIN 1 3
 CC FT TRANSMEM 4 24 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 89 113 POTENTIAL.
 CC FT TRANSMEM 119 139 PORE-FORMING (POTENTIAL).
 CC FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 172 192 POTENTIAL.
 CC FT DOMAIN 198 222 PORE-FORMING (POTENTIAL).
 CC FT TRANSMEM 235 255 POTENTIAL.
 CC FT DOMAIN 256 388 CYTOPLASMIC (POTENTIAL).
 CC FT CAROHYD 81 84 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CAROHYD 84 84 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT VARSPLIC 63 67 KILVE -> KAMAI (IN ISOFORM 2).
 CC FT VARSPLIC 68 398 MISSING (IN ISOFORM 2).
 CC SQ SEQUENCE 398 AA; 43051 MW; 478A834B78AEC92 CRC64;

Query Match 36.9%; Score 770.5; DB 1; Length 398;
 Best Local Similarity 49.8%; Pred. No. 8e-46;
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;

OY 42 MKKWTSTFLVYVYLLIIGAAVFKALEPOEISORTTIVIOKOTFIACHACVNSTELDE 101
 DB 1 MRSTLLALALVALIVSGALVFQALQEPHEQOAKKMDHGRDOFLRHPVCVSOKSLED 60
 OY 102 LIQOIVAAINAGIIP---LGNSNGVSHMDIGSSFFAGVITTTTIFGNSPTPEGKITF 158
 DB 61 FIKLLEVALGGGANPETSMTNSSNMSAMMGSAFFPSGIIITTYIGNVLTDTAGRL 120
 OY 159 CTVYALGIPLEGFLLAGVDDQGTGFGIAKVEDFTFKMNSQRIKRIITSTIFILG 218
 DB 121 CTVYALVGPILGFMLAGVDRGLSSLRGIGHIEAIFLKMHPPLVSLAVFLLLG 180
 OY 219 CULFVALPAVIRKHIKIGMSALDAIYFVVTITTTGFGDYVAGGSDIEYDFKPVVWMT 278
 DB 181 CLIFLFTPTFVSYSMSWKSLEAIFYIVITLTTFVGFYVPCDGTGQNSPAYQPLVWMT 240
 OY 279 LVGLAFYAVLSMIGDMLVISKTEEGEYGFRAHAEMTANTTA 323
 DB 241 LRGELAFYAVLTTTGNMLRAVSRKTRAEWGGLTAQAASMTGVTVA 285

RESULT 5
 CIMS HUMAN
 ID CIMS HUMAN STANDARD; PRT; 499 AA.
 AC 095279;
 DT 01-OCT-2000 (rel. 40, Created)
 DT 01-OCT-2000 (rel. 40, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACID-SENSITIVE POTASSIUM
 DE CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL 2).
 GN KCMK5 OR TASK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE-99030343; PubMed-9812978;
 RA Reyes R., Duprat F., Lesage F., Fink M., Salin P.A., Farnan N.,
 RA Lazdunski M.;
 RT Cloning and expression of a novel pH-sensitive two pore domain K+
 RT channel from human kidney.
 RL J. Biol. Chem. 273:30863-30869(1998).
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL
 CC K+ CONCENTRATIONS.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
 CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL
 CC ACIDIFICATION.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF084830; AAC79458.1; -.
 CC DR MIM: 603493; -.
 CC DR InterPro: IPR000099; -.
 CC DR InterPro: IPR001622; -.
 CC DR InterPro: IPR003280; -.
 CC DR Pfam: PF02034; TWIK_Channel; 1.
 CC DR PRINTS: PRO1333; 2PORECHANNEL.
 CC DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 CC Glycoprotein.
 CC FT DOMAIN 1 7
 CC FT TRANSMEM 8 26 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 85 112 POTENTIAL.
 CC FT TRANSMEM 113 133 PORE-FORMING (POTENTIAL).
 CC FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 158 180 POTENTIAL.
 CC FT DOMAIN 190 215 PORE-FORMING (POTENTIAL).
 CC FT TRANSMEM 230 250 POTENTIAL.
 CC FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).
 CC FT CAROHYD 77 77 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823DDA CRC64;

Query Match 20.1%; Score 420; DB 1; Length 499;
 Best Local Similarity 30.8%; Pred. No. 8.8e-26;
 Matches 105; Conservative 62; Mismatches 11; Indels 54; Gaps 11;

OY 54 VVLYIIGAAVFKALEPOEISORTTIVIOKOTFIACHACVNSTELDELIQOIVAAINAG 113

RX MEDLINE-97165959; PubMed-9013852;
 RA Lesage F., Lautitzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
 RA Lazdunski M.;
 RT "The structure, function and distribution of the mouse TWIK-1 K+
 RT channel.";
 RL FEBS Lett. 402:28-32(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SVJ; TISSUE=Liver;
 RX MEDLINE-98218573; PubMed-9559671;
 RA Arizhli I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;
 RT "Structure, chromosome localization, and tissue distribution of the
 RT mouse twik K+ channel gene.";
 RL FEBS Lett. 425:310-316(1998).
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
 CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
 CC EPIDIDYMUS, UTERUS, PLACENTA, COLON AND JEJUNUM, MODERATE
 CC EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
 CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
 CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
 CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
 CC CORTEX.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
 CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
 CC STABILIZES AFTER DAY 8.
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
 CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC -----
 DR EMBL AF033017; AAC16973.1; -;
 DR MGI:109322; Kcni1.
 DR InterPro: IPR000099; -;
 DR InterPro: IPR001622; -;
 DR InterPro: IPR001779; -;
 DR InterPro: IPR003280; -;
 DR Pfam: PF02034; TWIK_channel.1.
 DR PRINTS: PRO1096; TWIKCHANNEL.
 DR PRINTS: PRO133; 2PORECHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 21 41 POTENTIAL.
 FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 133 153 POTENTIAL.
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 178 198 POTENTIAL.
 FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 247 267 POTENTIAL.
 FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 336 AA; 38275 MW; A996060A18266FD4 CRC64;

Query Match 17.7%; Score 370; DB 1; Length 336;
 Best Local Similarity 28.9%; Pred. No. 1,5e-18;
 Matches 103; Conservative 72; Mismatches 128; Indels 54; Gaps 12;

OY 51 FLVAV--VLVLIIAAFAFKALKEPOEISORTTIIYIKOTFIAGHCANSTLDELIOOIVA 108
 DB 25 FLVAVGLVLIIVFAVAFSSSEELPYEDILKROELKRLRFLKEHCISEPOLDEOFLGAVLE 84

OY 109 AINAGIIPICLNSSNOVSHMDLGSSFFAGVITITIGCAN--ATEGKIFCIIVALLGIP 168
 DB 85 ASNVGVSVLSNASGN -WNMFSTALFPASTVLTSTYGHT--LSDGKACACIIYVIGIP 143
 OY 169 LFGFLAGVDQDLGTFGRKIAVEDFTFKMNSQTFIRI--FILPGVLPALP 226
 DB 144 FTLLFTALVQRTVHVTR--RPVLYFHIRMGFSKOYVAIVHVLGTFGVSCFEFF--P 199
 OY 227 AVIFKHEE-CMSALDAIFVIVITLTIGFGDYVAG-CSDIEYLDYFVPVFMVILVGLAY 284
 DB 200 AAFVSVLEDMMNLTSEYFPGFISLTIGLDYVPGEGYKNKRFELVYAGITCVLLGLIT 259
 OY 285 FAVLNMGIMGLVYISKRTKEVEGFRAHAAEWANVAE--TRRLSVEITDKQORAT 344
 DB 260 MLVVL-----ETCECELHEIK-----KFRKMF 280
 OY 345 SVRKLSAELAG--NNHQLTPCRRTLSVHNLISERVLP--LKAES-ITLNLGTPH 398
 DB 281 YVRKDKDEDLVHMEHQ--LSFSSVTEQVAGLKEEOKSEPFVASOSPVEDGSADH 336
 RESULT 8
 C1W3_HUMAN STANDARD; PRT; 394 AA.
 AC 014649;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM
 DE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
 GN KCNK3 OR TASK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE-97459932; PubMed-9312005;
 RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
 RT "Task, a human background K+ channel to sense external pH variations
 RT near physiological pH.";
 RL EMBL J. 16:5464-5471(1997).
 RN [2]
 RP ACTIVATION.
 RX MEDLINE-99254548; PubMed-10321245;
 RA Patel A.J., Honore E., Lesage F., Fink M., Reyes R., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore K+ in background K+
 RT channels.";
 RL Nat. Neurosci. 2:422-426(1999).
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
 CC CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
 CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
 CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
 CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST
 CC EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN,
 CC LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SPINAL INTESITINE AND COLON.
 CC -1- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY
 CC HALOTHANE AND ISOFLURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC -----
 DR EMBL AF006823; AAC51777.1; -;

DR MIM; 603220; -
 DR InterPro: IPR000099; -
 DR InterPro: IPR001622; -
 DR InterPro: IPR003092; -
 DR InterPro: IPR003280; -
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PRO1095; TASKCHANNEL.
 DR PRINTS: PRO1333; 2PORECHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KM Glycoprotein.
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 9 29 POTENTIAL.
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 108 128 POTENTIAL.
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 159 179 POTENTIAL.
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 223 243 POTENTIAL.
 FT DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
 SO SEQUENCE 394 AA; 43518 MW; 9FAC8266F15FB7 CRC64;
 Query Match 17.78; Score 370; DB 1; Length 394;
 Best Local Similarity 28.08; Pred. No. 1.8e-18;
 Matches 109; Conservative 66; Mismatches 126; Indels 88; Gaps 13;
 Oy 42 MKMWTSTIFLV--VYLIIIGAVFKALRPOEISORTTIVIKOTFIQAHACVNS--T 97
 Db 1 MKRONVTLALIVCTFTYLLVGAIVFDLSEPELIEKORIELKQDELKARYNLISGGYE 60
 Oy 98 ELDELIOQVIAINAGIIPLGSSNOVSHMDIGSFEFAGTIVITIGFNISPTTEGGKI 157
 Db 61 ELEVRVRL-KPKAGV-----QMFAGSFFAIVITITIGVGHAPPTDGGKV 108
 Oy 158 FCIIYALGIPFGLAGVDOIGTF-----GKIAYVEDTIFKWNVQTKIRI 208
 Db 109 FCMFYALGIPGLVPMQSGERINTLVRYLLHRAKKGGLRRAD-----VSM 156
 Oy 209 ISTIFILFGCVLPAVAFKIEGMSALDAIVFYITTTGFGVYAGGSD--IEY 266
 Db 157 ANMWLIGFSCISITLCIGAAAFSHYEMTPFOAYITITITIGFGDYALQDQALQT 216
 Oy 267 LDFFKPVWEMILGLAVFAVISMIGDWLNVISKTRKEV----- 307
 Db 217 QPVVASEFYIILGLVIGAFNLV--VLRETMNADEKRAHRLALTRNGAGGGG 274
 Oy 308 GEFANHAEMTA-----NVTAE-----FKETRRKISVEL----YDKF 340
 Db 275 GGGSAHTTDAASSTAAGGGGFRNVVAEVLHFOGMSCLWYKSRKLOYSIPMIPRDL 334
 Oy 341 QRATSVKRLKSLAELAGNHNOELTPCRRTL 369
 Db 335 TSDTCVDSHSSPGGGRYS-DTPSRKCL 362
 RESULT 9
 CIRM_MOUSE STANDARD; PRT; 409 AA.
 AC 035111; 035163;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM
 CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL)
 DE CARDIAC TWO-PORE BACKGROUND K+ CHANNEL (CTPAK-1).
 GN KINK3 OR TASK OR CTPAK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.

RC TISSUE=Heart;
 RA MEDLINE=98165556; PubMed=9506712;
 RX Kim D., Fujita A., Horio Y., Kurauchi Y.;
 RT "Cloning and functional expression of a novel cardiac two-pore
 RT background K+ channel (CTPAK-1).";
 RL Circ. Res. 82:513-518(1998).
 RN [2]
 RP SEQUENCE OF 4-409 FROM N.A.
 RX MEDLINE=97459932; PubMed=9312005;
 RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
 RT "TASK, a human background K+ channel to sense external pH variations
 RT near physiological pH.";
 RL EMBD J. 16:5464-5471(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=40287574; PubMed=10748056;
 RA Lopes C.M., Gallagher P.G., Buck M.E., Butic J., Goldstein S.A.;
 RT "Proton block and voltage gating are potassium-dependent in the
 RT cardiac leak channel Kcnk3.";
 RL J. Biol. Chem. 275:16969-16978(2000).
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
 CC CHANNEL PROTEIN, RECTIFICATION DIRECTION, RESULTS FROM POTASSIUM
 CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
 CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
 CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE, FEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED
 CC IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL
 CC INTESTINE AND STOMACH, NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
 CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
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 CC -----
 DR EMBL; AB008537; BAA25436.1; -
 DR EMBL; AF006824; AAC53367.1; -
 DR EMBL; AB013345; BAA28349.1; -
 DR EMBL; AF241798; AAF81418.1; -
 DR EMBL; AF242508; AAF81418.1; JOINED.
 DR MGD; MG1:100509; Kcnk3.
 DR InterPro: IPR000099; -
 DR InterPro: IPR001622; -
 DR InterPro: IPR003092; -
 DR InterPro: IPR003280; -
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PRO1095; TASKCHANNEL.
 DR PRINTS: PRO1333; 2PORECHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KM Glycoprotein.
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 9 29 POTENTIAL.
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 108 128 POTENTIAL.
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 159 179 POTENTIAL.
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 223 243 POTENTIAL.
 FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 4 4 O -> E (IN REF. .)
 FT CONFLICT 123 123 V -> I (IN REF. .)
 SO SEQUENCE 409 AA; 45068 MW; 35236011AAC577 CRC64;

RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
 RA Mehta Y., Forsythe J.R., Yost C.S.,
 RT "TWIK-2, a new weak inward rectifying member of the tandem pore domain
 RT potassium channel family.";
 RL J. Biol. Chem. 274:7887-7892(1999).
 RN [3]
 RP ERRATUM.
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
 RA Mehta Y., Forsythe J.R., Yost C.S.,
 RL J. Biol. Chem. 274:24440-24440(1999).
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
 CC TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
 CC PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED
 CC IN PERIPHERAL BLOOD LEUCOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
 CC LOWEST EXPRESSION DETECTED IN BRAIN.
 CC -1- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL
 CC DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARBITUM.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
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 CC -----
 DR EMBL: AF134149; AAD22980.1; -;
 DR EMBL: AF117708; AAD24000.1; -;
 DR MIM: 603939; -;
 DR InterPro: IPR001622; -;
 DR InterPro: IPR001779; -;
 DR PRINTS: PRO1096; TWIK1CHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 5 25 PORE-FORMING (POTENTIAL).
 FT DOMAIN 90 115 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 121 141 PORE-FORMING (POTENTIAL).
 FT DOMAIN 142 172 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 173 193 PORE-FORMING (POTENTIAL).
 FT DOMAIN 199 223 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 236 256 PORE-FORMING (POTENTIAL).
 FT DOMAIN 257 313 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 53 53 C->A: NO CHANNEL ACTIVITY.
 SQ SNOUCE 313 AA; 33747 MW; 1379382DFB057SDE CRC64;

Query Match 16.48; Score 342; DB 1; Length 313;
 Best Local Similarity 34.48; Pred. No. 1.1e-16;
 Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;

OY 57 YLITGAFALEPOEPOISORTTIVIOKOTIFIAQHACVNSTEIDELIQOYAATNAGIIP 116
 DB 17 YLVIGALLVLRLEGPHEARLAELETLRADLORSPCVAPADAFERYVLAAGRLGRV 76
 OY 117 LGNSNNOVS---HWDGSSFFAGVITITIGFNGISPRTEGGKIFCIIVALLGIPLEGF 172
 DB 77 LANSSGANSNDPAMDFASALFPASTILITVGYCTTPLDAGKAFSIAFALLGCVPTTML 136
 OY 173 LLAGVGDLGTITGKIAKVEDFIKNNVSQTKIRIISTIIIFLGGCVLEVA--LPAVIF 230
 DB 137 LITASQRLSL---LTHVPLSLMRMGWDPRACRMLVALLGVAVTVCFVPAVIF 192
 OY 231 KHI-EGMSALDAIVFVITITITGFGDYVAGSDIE-YLDFYKRVVWFILVGLATYAAV 288
 DB 193 AHLEEASFLDAFYCFPISTLSTIGLDGYVPGEGAPYRALYKVLVIVYVFLGLVAVLV 252

OY 289 L 289
 DB 253 L 253

RESULT 12
 ORK1_DROME STANDARD; PRT; 1001 A;
 ID ORK1_DROME
 AC 094526;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (A TWO PORE DOMAIN POTASSIUM
 DE CHANNEL ORK1).
 GN ORK1 OR CG1615.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Schizophora; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LETTA;
 RX MEDLINE=97075152; PubMed=8917578;
 RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Busch M.H.,
 RT "ORK1, a potassium-selective leak channel with two pore domains
 RT cloned from Drosophila melanogaster by expression in Saccharomyces
 RT cerevisiae";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoek R.R., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H., Blazer R.G., Olmpe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews L., Binkov C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktar S.L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhand J., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu I., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport J., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrara S., Fleischmann W.,
 RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei K.-H., Ideyem C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kevinson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matrei B., McIntosh T.C., McLeod M., McPherson D.,
 RA Merkulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Wu D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard D., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Sotter E., Spradling A.C., Stapleton M., Strick R., Sun E.,
 RA Stryckas R., Teeter C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassenaar D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu I., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: BACKGROUND POTASSIUM CHANNEL. RECTIFICATION IS DEPENDENT

DR EMBL: AF012324; AAF21603.1; -
 DR EMBL: AF158234; AAF14528.1; -
 DR MGD: MG1:1341841; Kcnk8.
 DR InterPro: IPR001622; -
 DR InterPro: IPR003280; -
 DR PRINTS: PR01333; 2PORECHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KM Glycoprotein.
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 11 31 POTENTIAL.
 FT DOMAIN 92 118 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 120 140 POTENTIAL.
 FT DOMAIN 141 172 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 173 193 POTENTIAL.
 FT DOMAIN 199 227 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 233 253 POTENTIAL.
 FT DOMAIN 254 307 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 1 3 MGS -> TR (IN REF. 4).
 FT CONFLICT 2 3 GS -> TR (IN REF. 4).
 FT CONFLICT 84 84 G -> S (IN REF. 2, 3, 4 AND 5).
 FT CONFLICT 231 232 YH -> SP (IN REF. 2).
 FT CONFLICT 293 293 T -> P (IN REF. 2).
 SQ SEQUENCE 307 AA; 32168 MW; 567D32AE35BA44F CRC64;

Query Match 14.6% Score 305.5; DB 1; Length 307;
 Best Local Similarity 29.6%; Pred. No. 3.5e-14;
 Matches 84; Conservative 65; Mismatches 94; Indels 41; Gaps 12;

QY 44 WKTVSTFLVNVLLIIGAFAFKALEQPEISORTTIVITOKETIAOH-ACVNSTELDEL 102
 7 WARYLLMLAMLLMAGAVVLALEGPRARHQAQOAEALASQAERHACLPPEALEEL 66
 103 IQQVAAIMAGIIPLGSSNOVSHMDLGSFFPAGTVITTTGFGNISRTGKICITY 162
 67 LGVALRAQAHGVSSLGNGS-ETSMWMDLPALLFTASILTITTYGOMAPLSSGKAFVCVY 125
 QY 163 ALLGIPLEGFLIAGVQDGLTIF--GKGIKVEDTPIKNNVSOPTKRIITTI-IFILFG 218
 126 AALDLPASLALVALRHCLPFLVSRPGDWVA-----IRKOLAPQAALALQAGLGLVA 179
 QY 219 CVLEFVALPAVIFKHIEG-WSALDAIFYVITLTITIGFGDVY-AGGSDELYDFFKPVWF 276
 180 CV-FMLPALTALVMGVGQCSLLLEAIFCFGSLSTIGLDLIPAHGRGLH-----PATYH 232
 QY 277 -----WILVGLAIFRAVLSMIGDMLRVISKTKKEVGEFRA 312
 233 LGQFALLGLYLLGL-----LAML-----LAVETFSELPOVRA 264

RESULT 14
 C1W7_HUMAN STANDARD; PRT; 307 AA.
 AC G9Y2U2; G9Y2U4; G9Y2U3;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 7.
 GN KCNK7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=99223496; Pubmed=10206991;
 RA Salinas M., Reyes R., Lesage F., Fosset M., Heurteaux C., Romey G.,
 RA Lazdunski M.;
 RT "Cloning of a new mouse two-pore domain channel subunit and a human
 homologue with a unique pore structure.";

RL J. Biol. Chem. 274:11751-11760(1999).
 CC -1- FUNCTION: PROBABLE POTASSIUM CHANNEL SUBUNIT. NO CHANNEL ACTIVITY
 CC OBSERVED IN VITRO AS PROTEIN REMAINS IN THE ENDOPLASMIC RETICULUM.
 CC MAY NEED TO ASSOCIATE WITH AN AS YET UNIDENTIFIED PARTNER IN ORDER TO
 CC REACH THE PLASMA MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE. E1N (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A (SHOWN HERE), B AND C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
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 CC -----
 DR EMBL: AF110522; AAD29578.1; -
 DR EMBL: AF110524; AAD29580.1; -
 DR EMBL: AF110523; AAD29579.1; -
 DR MIM: 603940; -
 DR InterPro: IPR001622; -
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KM Glycoprotein; Alternative splicing.
 FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 11 31 POTENTIAL.
 FT DOMAIN 92 119 PORE-FORMING (POI:VITAL).
 FT TRANSSEM 120 140 POTENTIAL.
 FT DOMAIN 141 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 171 191 POTENTIAL.
 FT DOMAIN 199 227 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 233 253 POTENTIAL.
 FT DOMAIN 254 307 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 241 252 YLLGLLAMLALA -> GTSISLGTAWBG (IN ISOFORM B).
 FT VARSPLIC 253 307 MISSING (IN ISOFORM B).
 FT VARSPLIC 241 257 YLLGLLAMLAVTPS -> KSSHLTACGGRKRSID
 FT VARSPLIC 258 307 MISSING (IN ISOFORM C).
 SQ SEQUENCE 307 AA; 31946 MW; BD4A36DD9591AD CRC64;

Query Match 14.4% Score 300.5; DB 1; Length 307;
 Best Local Similarity 29.9%; Pred. No. 7.6e-14;
 Matches 88; Conservative 60; Mismatches 111; Indels 35; Gaps 10;
 QY 44 WKTVSTFLVNVLLIIGAFAFKALEQPEISORTTIVITOKETIAOH-ACVNSTELDEL 102
 7 WSRVGLLVVAHLMLAGAVVFALEGPACRIQAELEAEI VQAEHRACLPALGAEEL 66
 103 IQQVAAIMAGIIPLGSSNOVSHMDLGSFFPAGTVITTTGFGNISRTGKICITY 162
 67 LGTALAQAHGVSTLGNGS-EGRTWMDLPALLFTASILTITTYGMAPLSSGKAFVCVY 125
 QY 163 ALLGIPLEGFLIAGVQDGLTIFPKGIKVEDTPIKNNV-ITKRIITTIIFILEGCVLF 222
 126 AALDLPASLALVALRHCLPFLVSRPGDWVA---VHML-PAARALALQAGLGLVSSF 182
 QY 223 VALPAVIFKHIEG-WSALDAIFYVITLTITIGFGDVYAG-GSDELYDFFKPVWF----- 276
 183 VLLPALTALVMGVGQCSLLGAVYFCFSSLSITIGLDLIPG VRSLLH-----PVIYHIGQL 236
 QY 277 -----WILVGLAIFRAVLSMIGDMLRVISKTKKEVGEFRA/IAAEW--TANVTAE 324
 237 ALLGIPLEGFLIAGVQDGLTIFPKGIKVEDTPIKNNV-ITKRIITTIIFILEGCVLF 278
 RESULT 15
 TOKI_YEAST

ID TOK1_YEAST STANDARD; PRT; 691 AA.
AC P40310; 005721;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTWARD-RECTIFIER POTASSIUM CHANNEL TOK1 (TWO-DOMAIN OUTWARD RECTIFIER
DE K+ CHANNEL YORK).
DE TOK1 OR DUK1 OR YJL093C OR J0911.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95076716; PubMed=7985424;
RA Miosga T., Witzel A., Zimmermann F.K.;
RT "Sequence and function analysis of a 9.46 kb fragment of
RT Saccharomyces cerevisiae chromosome X.";
RL Yeast 10:965-973(1994).
RN 12
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=NY13;
RX MEDLINE=95379951; PubMed=7651518;
RA Ketchum K.A., Joiner W.J., Sellers A.J., Kaczmarek L.K.,
RA Goldstein S.A.N.;
RT "A new family of outwardly rectifying potassium channel proteins with
RT two pore domains in tandem.";
RL Nature 376:690-695(1995).
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=96303826; PubMed=8723646;
RA Reid J.D., Lukas W., Shafatlian R., Bertl A., Scheurmann-Ketter C.,
RA Guy H.R., North R.A.;
RT "The S. cerevisiae outwardly-rectifying potassium channel (DUK1)
RT identifies a new family of channels with duplicated pore domains.";
RL Recept. Channels 4:51-62(1996).
RN 14
RP SEQUENCE FROM N.A.
RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M.,
RA Romy G., Barhanin J.;
RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
CC 1- FUNCTION: OUTWARDLY RECTIFYING POTASSIUM CHANNEL.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC 1- DOMAIN: SEEM TO BE COMPOSED OF TWO PORES.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
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CC
CC EMBL; X77087; CAA54360.1; -
CC EMBL; Z49368; CAA89386.1; -
CC EMBL; U28005; AAC49070.1; -
CC EMBL; X94403; CAA64176.1; -
CC EMBL; U37254; AAC49168.1; -
CC DR PIR; S46585; S46585.
CC DR PIR; S47058; S47058.
CC DR SCD; S0003629; TOK1.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel.
FT TRANSMEM 72 92
FT TRANSMEM 138 158
FT TRANSMEM 171 191
FT TRANSMEM 204 224
FT TRANSMEM 247 266
FT TRANSMEM 302 322
FT TRANSMEM 380 400
FT TRANSMEM 436 456
FT TRANSMEM 442 462
FT TRANSMEM 512 532
FT CONFLICT 512 532
FT E -> G (IN REF. 3).
FT E -> G (IN REF. 3).

SQ SEQUENCE 691 AA; 77407 MW; 507167E487B77AAJ CRC64;
Query Match 10.4%; Score 217; DB.: Length 691;
Best Local Similarity 23.2%; Pred. No. 9, 1e-08;
Matches 99; Conservative 58; Mismatches 135; Indels 134; Gaps 18;
OY 20 LSPSSKPTVLASRVESDSAINVMKKTGSTIFLWVLLYLITICAAVFKALEPOEISORTT 79
DB 158 LHRSKRLTYIKSQL-----INITGMTIAGMILVDYI-----VCSLNDMP----- 198
OY 80 IVIOKOTFLAQHACVNSTELDELIOQIVAIN-----AGII-----LGNSNOVS----- 125
DB 199 --IYSKTIGFWFACISSGLY--LVCTIITLTHPIGYKLCNYFTFPLNPNERSIMAYVL 254
OY 126 -----HMDGSSFFPAGVYITIGGNISTIEGKRICITIALGILP 169
DB 255 LSLMLIWGAGMFSGLLHITYGNALYCTVSLTVGLGDIISVGAKIMVLIPLFSLGVAL 314
OY 170 FGFL-----AGVDOLGTIF-----GKGIKVEDTFIKW-----NVSQTRIRIISTT 212
DB 315 MGLIVMTSIIQKSSGPIFFHRYVEKGRK-----SNKVVYDSSKNLSERE----- 361
OY 213 IFILFCV-----LEVA-----LPAVH-----GMSALDAIFYVITLT 251
DB 362 AFDLMKCIROTASRKQHWESLSVTIAIFMAFWLGLALFVNAZMNSFYNCIYFCFLLT 421
OY 252 IGRGDYV-----AGSDIEYLDFFKPYWFWILVGLAFVAVVLSMIDMLRVISKTRKEY 307
DB 422 IGRGDYAPRTGAG-----RAFFVWALGAVPLMG--LSTVGDLLEIDISTSLDIKI 471
OY 308 GEF-----RAHAEWTAANYTAERKETRRRLSVIYKFORATSVKRLSAELA 355
DB 472 GESFNKKVYSIYVNGORALSEVMVNTGEIFEE-----DIAFGLEENTTSOSSQISEFN 527
OY 356 GNNHNE 361
DB 528 DNNSEE 533

Search completed: August 28, 2001, 17:13:14
Job time: 408 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:12:45 ; Search time 54.36 Seconds

(without alignments)
1000.319 Million cell updates/sec

Title: US-09-503-089a-4

Perfect score: 2090
Sequence: 1 MAAPDLDPKSAQNSKPRRL.....LNGLTPHCAGEDIAVIENMK 411

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_16: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organellar: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_unclassified: *
13: sp_vertebrate: *
14: sp_virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2044	97.8	411	4 Q9NRT2	Q9NRT2 homo sapien
2	1256.5	60.1	538	11 Q9H54	Q9H54 rattus norv
3	1251.5	59.9	538	4 Q9H59	Q9H59 homo sapien
4	499.5	23.9	294	4 Q9H591	Q9H591 homo sapien
5	409	19.6	502	11 Q9TK62	Q9TK62 mus musculu
6	375.5	18.0	336	11 Q9ZT2	Q9ZT2 rattus norv
7	351.5	16.9	259	6 Q02821	Q02821 oryctolagus
8	351.5	16.8	330	4 Q9HBC8	Q9HBC8 homo sapien
9	351.5	16.8	365	11 Q9H58	Q9H58 cavla porce
10	344	16.5	299	11 Q9QX34	Q9QX34 mus musculu
11	343.5	16.4	330	4 Q9H427	Q9H427 homo sapien
12	343	16.4	329	5 Q9H795	Q9H795 caenorhabd1
13	342.5	16.4	374	4 Q9NPC2	Q9NPC2 homo sapien
14	338.5	16.2	229	4 Q9H592	Q9H592 homo sapien
15	338	16.2	313	11 Q9ERU5	Q9ERU5 rattus norv
16	335	16.0	395	11 Q9H1D4	Q9H1D4 rattus norv
17	329.5	15.8	336	5 Q17185	Q17185 caenorhabd1
18	322.5	15.4	237	11 Q9ES08	Q9ES08 rattus norv
19	309.5	14.8	343	11 Q9J114	Q9J114 mus musculu

20	308.5	14.8	430	4 Q9H515	Q9H515 homo sapien
21	307	14.7	430	11 Q9ERS1	Q9ERS1 rattus norv
22	306	14.6	340	5 Q9VHE0	Q9VHE0 drosophila
23	304.5	14.6	398	5 Q9VFS9	Q9VFS9 drosophila
24	294.5	14.1	392	11 Q9ESM5	Q9ESM5 rattus norv
25	289	13.8	383	5 Q21094	Q21094 caenorhabd1
26	287	13.7	405	11 Q9ERS0	Q9ERS0 rattus norv
27	286.5	13.7	364	5 Q96790	Q96790 caenorhabd1
28	284	13.6	385	5 Q9VYX5	Q9VYX5 drosophila
29	279.5	13.4	408	4 Q9H14	Q9H14 homo sapien
30	279.5	13.4	461	5 Q9TP8	Q9TP8 caenorhabd1
31	279	13.3	393	5 Q9XU07	Q9XU07 caenorhabd1
32	271	13.0	392	5 Q9NEV3	Q9NEV3 caenorhabd1
33	270.5	12.9	522	5 Q22042	Q22042 caenorhabd1
34	269	12.9	325	5 Q18120	Q18120 caenorhabd1
35	266	12.7	1910	5 Q22426	Q22426 caenorhabd1
36	263	12.6	452	5 Q93531	Q93531 caenorhabd1
37	256.5	12.3	385	5 Q9V362	Q9V362 drosophila
38	252.5	12.1	1539	5 Q19611	Q19611 caenorhabd1
39	247	11.8	444	5 Q45891	Q45891 caenorhabd1
40	246	11.8	389	5 Q9VE68	Q9VE68 drosophila
41	245.5	11.7	513	5 Q22940	Q22940 caenorhabd1
42	244.5	11.7	270	11 Q9H157	Q9H157 cavla porce
43	243.5	11.7	427	5 Q23386	Q23386 caenorhabd1
44	237	11.3	643	5 Q9XXF6	Q9XXF6 caenorhabd1
45	236	11.3	550	5 Q93764	Q93764 caenorhabd1

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	411 AA.
Q9NRT2	Q9NRT2			
ID	Q9NRT2			
AC	Q9NRT2			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.			
GN	TREK-1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain; Benham C.D., Cairns W., Gloger J.S., Jennings C.,			
RA	Meadows H.J., Murdoch P., Chapman C.G.,			
RA	Medhurst A.D.,			
RT	"Cloning, localization and functional expression of the human ortholog of the TREK-1 potassium channel."			
RL	Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF171068; AAF89743.1;			
DR	InterPro: IPR001622;			
DR	InterPro: IPR003280;			
DR	PRINTS: PR01333; ZPROKCHANEL.			
KW	Ionic channel.			
SO	SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42; CRC64;			

Query Match	97.8%;	Score 2044;	DB 411	Length 411;
Best Local Similarity	96.4%;	Pred. No. 1e-11;		
Matches 396;	Conservative 11;	Mismatches 11;	Indels 0;	Gaps 0;
OY	1 MAAPDLDPKSAQNSKPRRLSFSKPTVLASRVESDSALINWKIVSTFLVYVLLIT 60			
DB	1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDTINWAKIVSTFLVYVLLIT 60			
OY	61 GAIVFALKEQPELSQFTTVIOKQFIQAHCNSLFEILLOQIVAAINAGIIPGNS 120			
DB	61 GAIVFALKEQPELSQFTTVIOKQFIQAHCNSLFEILLOQIVAAINAGIIPGNT 120			
OY	121 SNQVSHMDLSSFFFACTVITIGFGNISPRTEGKITVAVLGIPEFGFLAGVDQ 180			

Db	121	SNQISHMLOGSSFFPAGVITITIGFNISPTBEGKIFCTITAYLLGIPGLLAGVDQ	180
Qy	181	LGTFEGKGLAVEEDPLIKMANSQRIKIIISTITIFLGCYLVNLPVIRKIHIEGMSALD	240
Db	181	LGTFEGKGLAVEEDPLIKMANSQRIKIIISTITIFLGCYLVNLPVIRKIHIEGMSALD	240
Qy	241	AIYFVYITLTITIGFDYVAGSDIEYLDYFKPVVFMILVGLVFAAVLSMIGDMLRVIS	300
Db	241	AIYFVYITLTITIGFDYVAGSDIEYLDYFKPVVFMILVGLVFAAVLSMIGDMLRVIS	300
Qy	301	KKTKEEVGEFRAHAAEMWTANTYAEFKETRRLSVEIDKFORATSVYKRSIAELAGNHQ	360
Db	301	KKTKEEVGEFRAHAAEMWTANTYAEFKETRRLSVEIDKFORATSVYKRSIAELAGNHQ	360
Qy	361	ELTPCRRLTSVNNHLSPEEVPYPLIKKESITYLNGTTPHCGEDVLAENNRK	411
Db	361	ELTPCRRLTSVNNHLSPEEVPYPLIKKESITYLNGTTPHCGEDVLAENNRK	411

RESULT 2

AD	09JISA	PRELIMINARY;	PRT;	538 AA.
AC	09JISA			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, last annotation update)			
DE	POTASSIUM CHANNEL TREK-2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20298807; PubMed=10747911;			
RA	Bang H., Kim Y., Kim D.;			
RT	"TREK-2, a new member of the mechanosensitive tandem-pore K ⁺ channel family.";			
RL	J. Biol. Chem. 275:17412-17419(2000).			
DR	EMBL; AF196965; AAF75132.1; -.			
DR	InterPro; IPR000099; -.			
DR	InterPro; IPR001622; -.			
DR	InterPro; IPR003280; -.			
DR	Pfam; PF00234; TWIK_CHANNEL.1.			
DR	PRINTS; PR01333; 2PORECHANNEL.			
SO	SEQUENCE 538 AA; 59600 MW; 1FF33FOA52B97E4 CRC64;			

```
Dd      392 LRVLSKKKEEVGELKHAAMKANVVAEFPETRRRLSV *IDLRQAATIRSMERRRLG 381
Qy      352 AELAGNNHNOELLPCRTLL 369
Db      382 LDGRAHSYLDMLSPPKRSV 399
```

RESULT	3
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ID	ORGANISM	PRELIMINARY	PERT	538 AA
AC	09HB59			
AC	09HB59			
DT	01-MAR-2001 (TREMBlrel, 16, Created)			
DT	01-MAR-2001 (TREMBlrel, 16, Last sequence update)			
DT	01-MAR-2001 (TREMBlrel, 16, Last annotation update)			
DE	2P DOMAIN POTASSIUM CHANNEL, TREK2.			
GN	KCNK10.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertei; ia; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homi; idae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20435789; PubMed=10880510;			
RA	Lesage F., Terrenoire C., Roney G., Lazdunski J.			
RT	"Human TREK2, a 2P domain mechano-sensitive K ⁺ channel with multiple			
RT	regulations by polyunsaturated fatty acids, 1-phospholipids and Gs.			
RT	G1, and Gq protein-coupled receptors."			
RL	J. Biol. Chem. 275:28398-28405(2000).			
DR	EMBL; AF279890; AAG15191.1;			
KW	Ionic channel			
SO	SEQUENCE 538 AA; 59764 MW; 8EA615B08D147F; CRC64;			

Query Match

[illegible]

QY 169 LFGFLLAGVGDGLTIFGKIAKVEDTFIKMNSQTKIRIITII--FILEGCVLEVALP 226
 DB 144 FTLLFTFAVQRTVAVTR--RPVLYFHWRGFSKQVAVIAVHVLGLTVCSCFFPIPA 199
 QY 227 AVTEFKIEE-GMSALDAIYFVITLTITIGFDYVAG-GSDIEYIDFKPVVWMIIVGLAY 264
 DB 200 AAFVSELEDDMNFLSEYFCFISLTIGLGDYVPGEGYNOKFRELYKIGITCYLLGLIA 259
 QY 285 FAVALSMIDMLRVLSK-----KTRKEGVEFRAHAAE 316
 DB 260 MLVLETFCE-LHELKFFRKMFEYKKDKEDQVHME 295

RESULT 7
 ID 002821 PRELIMINARY: PRT: 259 AA.
 AC 002821:
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DE DOUBLE PORE POTASSIUM CHANNEL RABCKNK1 (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Orlas M., Velazquez H., Tung F., Desir G.V.;
 RL Submitted (May-1997) to the EMBL/Genbank/DDb databases.
 DR EMBL: AF004695; AAB61602.1; -
 DR InterPro: IPR001622; -
 DR InterPro: IPR001779; -
 DR InterPro: IPR003280; -
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR PRINTS: PR01096; TWIKCHANNEL.
 FT NON_TER 1 259
 FT NON_TER 1 259
 SQ SEQUENCE 259 AA; 29311 MW; 5546ABBD278E79F3 CRC64;

Query Match 16.8%; Score 353.5; DB 6; Length 259;
 Best Local Similarity 33.1%; Pred. No. 2.7e-18;
 Matches 78; Conservative 57; Mismatches 94; Indels 7; Gaps 5;
 QY 51 FLVAV--VLVLIIGAFAFKALEPOEISQRTTYIYOKOTFIAGACVNSTELDELICQIYA 108
 DB 26 FLVGLVLTIVGAVVSEVELPEYEDLRLQELRKLRRVEHECHLSBOOLEFLGRVLE 85
 QY 109 AINAGIIPLGNSNOVSHMDLSSFFACTVITTTIGFNGISPRTEGKIFCIITALLGIP 168
 DB 86 ANNYGVSVSNASGN--WNWDFASALFPAFTVLTGTGHTVPLSDVGAFCIITVYIGIP 144
 QY 169 LFGFLLAGVGDGLTIFGKIAKVEDTFIKMNSQTKIRIITIIIFLPGCVLEVALP 228
 DB 145 FTLLFTFAVQRTVAVTR--RPVLYFHWRGFSKQVAVIAVHVLGLTVCSCFFPIPA 202
 QY 229 IFKHIE-GMSALDAIYFVITLTITIGFDYVAG-GSDIEYIDFKPVVWMIIVGL 282
 DB 203 VFSVLEDDMNFLSEYFCFISLTIGLGDYVPGEGYNOKFRELYKIGITCYLLGL 258
 RESULT 8
 ID 09HBC8 PRELIMINARY: PRT: 330 AA.
 AC 09HBC8:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE TWO PORE POTASSIUM CHANNEL KTS3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina V., Pountney D.,
 RA Koetsee W., Rudy B.;
 RT "KTS.2 and KTS.3 Two Novel Human Two Pore K+ Channels Closely Related
 RT to TASK1.";
 RL Submitted (APR-2000) to the EMBL/Genbank/DDb databases.
 DR EMBL: AF257081; AAG3127.1; -
 SO Ionic channel.
 SQ SEQUENCE 330 AA; 36130 MW; AA2A54D0615BC5 CRC64;

Query Match 16.8%; Score 351.5; DB 11; Length 330;
 Best Local Similarity 35.0%; Pred. No. 5.2e-18;
 Matches 91; Conservative 44; Mismatches 11; Indels 31; Gaps 8;
 QY 50 IFVLVLYLIIIGAFAFKALEPOEISQRTTYIYOKOTFIAGACVNSTELDELICQIYA 109
 DB 11 LVLCITCYLLVGAFAVDALAESEAE-SGRORLIVOKRGAL--FEGFAEDYRELERLALQA 69
 QY 110 --INAGIIPLGNSNOVSHMDLSSFFACTVITTTIGFNGISPRTEGKIFCIITALLGIP 167
 DB 70 EHRAG-----RQKPFQSYFAITVITTTIGYVAPGTDGSKVFCFVALLGI 118
 QY 168 PLFGFLLAGVGDGLTIFGKIAKVEDTFIKMNSQTKIRIITIIIFLPGCVLEVALP 226
 DB 119 PLTVTFQSLGERLNAVVRLLAAKCCGLRWTGVSTE--NLVAVGLACATLALG 174
 QY 227 AVTEFKIEE-GMSALDAIYFVITLTITIGFDYVAGSDIF--PYKRVWF--WIIYGLA 283
 DB 175 AAFSHFEGWTFEFAHYCYFILTITIGFDVVALQSG--RKLIPVAFSLYLLGLT 233
 QY 284 YFAVLSMI-----GDM 295
 DB 234 VIGAFINLVLEPLVASADM 253

RESULT 9
 ID 09JL58 PRELIMINARY: PRT: 365 AA.
 AC 09JL58:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE POTASSIUM CHANNEL TASK3.
 GN KCN9.
 OC Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN:
 RX MEDLINE-20287530; PubMed-10747866;
 RA Rajan S., Wismeyer E., Liu G.X., Preisig-Meyer R., Daut J.,
 RA Karschin A., Derst C.;
 RT "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
 RT extracellular histidine as pH sensor.";
 RL J. Biol. Chem. 275:16650-16657(2000).
 DR EMBL: AF212827; AAF63706.1; -
 DR InterPro: IPR000099; -
 DR InterPro: IPR001622; -
 DR InterPro: IPR003092; -
 DR InterPro: IPR003280; -
 DR Pfam: PF02034; TWIK_channel.1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR PRINTS: PR01095; TASKCHANNEL.
 SQ SEQUENCE 365 AA; 40769 MW; 261DC973FF53AF91 CRC64;

Query Match 16.8%; Score 351.5; DB 11; Length 365;
 Best Local Similarity 30.1%; Pred. No. 5.9e-18;
 Matches 94; Conservative 59; Mismatches 110; Indels 49; Gaps 9;


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DR EMBL; AF083652; AAC32863.1; -.
DR InterPro; IPR000099; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR003260; -.
DR Pfam; PF02034; TWIK_channel; 1
DR PRINTS; PRO1333; 2PORECHANNEL.
KW Ionic channel.
SQ
SEQUENCE 329 AA: 36992 MW:
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Query Match	16.48;	Score 343;	DB 5;	Length 329;
Best Local Similarity	34.18;	Pred. No. 2.1e-17;		
Matches 94;	Conservative 53;	Mismatches 95;	Indels 34;	Gaps 11;

```

OY      MKKATVSIFELV--VLYIIIGAFAFALROPOEISORTITVIOKOFIHOACVNSTEL 99
         ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 MKRONIRLSIYCTLYIIYLLVGAFAFPALEETENIILOKRLVORREKTKRYMNSN-DY 59

OY      100 DELIQIYAAL--NAGIIPJGNSNOVSHMDLGSSFEFFAGTVITTTIGEGNI 157
         ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      60 EILEEATTVKSVPHRAGY-----OKMFGSAGFEATTVITTTIGYSTPMTDAGK 108

OY      158 FCIIYALIGIPFGLFLLAGVDOGLTITFGIAVDEPTFKMWN50RKIIITIIIFILF 217
         ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      109 FCMYALAGITPLGLIMQSIGTERNNTPRAKL-----RFTIRRAKQOPITSSDLIIECT 163

OY      218 GC-VLEVALPAVIRKHTIEGMSALDAIEVVYITTTTIGFGYVA---GGS---DIEYLEDY 270
         ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      164 GWGGLLIFGAGFMESYENNTYFPAVYVYCFVTLTTTIGFGYVALOKRGSLOTPQEVY-FF 222

OY      271 KPYVWEITVLGALFAAVLMSIGMWLEKVIKSKREE 306
         ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      223 SLV---FLLFGLTVISAMNLL--VLFPLFMNEDE 253

```

RA Chapman C.G., Meadows H.J., Godden R.J., Cartledge D.A., Duckworth M.
R1 Keissell R.E., Murdoch P.R., Randall A.D., Rees G.I., Glover I.S.,
R2 "Cloning, localisation and functional expression of a novel human,
R3 cerebellum specific, two pore domain potassium channel".
R4 Brain Res. Mol. Brain Res. 82:74-83(2000).
R5 EMBL, AF279809; AAE95982.1; -
R6 EMBL, AF212829; AAE63708.1; -
R7 EMBL, AF257080; AAG33126.1; -
R8 EMBL, AF248241; AAG31730.1; -
R9 InterPro: IPR000099; -
R10 InterPro: IPR001622; -
R11 InterPro: IPR003092; -
R12 InterPro: IPR003280; -
R13 Pfam: PF002034; TWIK_channel; 1.
R14 PRINTS: PR01333; 2PORKCHANNEL.
R15 PRINTS: PR01095; TASKCHANNEL.
R16 Ionic channel.
R17 SEQUENCE 374 AA; 42263 MW; 8A19EAEE5A411...38 CRC64;

Query Match	16.48;	Score 342.5;	Length 374;
Best Local Similarity	26.58;	Pred. No. 2.7e-7;	
Matches 104;	Conservative 78;	Mismatches 147;	Indels 63; Gaps 12

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0Y 42 MKMKVSYIPIWV--VYLIIGAAVFALEPOBISORTI V4OKOFIIOHMCVNSTEL 99
Db 1 MKROVVRSLIYCTEFTYLLIGAAVFDLSEDHMBREFI--AEIRIKKRYN-ISEEDY 59
0Y 100 DELIOOIYVA--INAGIIPLGNSSNOVSHMDLGSPFFA LTTITFGNISPTREGKI 157
Db 60 ROLEVLIIQSEPHRAGV-----QMKFASPFYA LTTITGYHAAPGTAGKA 108
0Y 158 FCIIYALIGIPLEFGLIAGVDDLGITFGKIAKVEDTF LTTNSQIKIRI 208
Db 109 FCMFPAVIGIPLTVMFOSLGERM-----MTFV LKRIKCCGMNPDVSM 156
0Y 209 ISTIIFILFGVLEVALPAVIEKHIEGMSALDIYEVII ITGEGDYVA--GGSIDEX 266
Db 157 ENMYTVGFSCMGITLCIGAAAFSCOEESFPFHAYICPII ITGIFEDYVALOTKGALOK 216
0Y 267 LDFYKPVVWFILIVGLAYFAAVLISMIGDMLRVISKRTKEE VGEFPAHVA---EWTAN 320
Db 217 KPIYVAFSEFMIIIVGLTYIGAFNLV--VLRFLIMNDEDEI DAEERKASIALGNNSAVIH 274
0Y 321 VTAEFKETRRLSVEI-----YDKFORATSVK ILSAELAGNHOELTPCR 366
Db 275 IPEERPRPRPRYKADVDPLDQVSCCTCYRSDQYCGRSRVAQPN SFSALADPHYHSIS--Y 332
0Y 367 RTLVSNHLTSREVLVPLLRKAEIYINGLTPH 398
Db 333 KIEELISPTLNSLFPSPDISSISGLHSFIDH 364

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:05:47 ; Search time 47.95 Seconds

(without alignments)
498.141 Million cell updates/sec

Title: US-09-503-089A-5

Perfect score: 2042
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSPFGMLKRSSV 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_0601:*

- 1: /SID58/gcgdata/geneseq/geneseqp/AA1980.DAT:*
- 2: /SID58/gcgdata/geneseq/geneseqp/AA1981.DAT:*
- 3: /SID58/gcgdata/geneseq/geneseqp/AA1982.DAT:*
- 4: /SID58/gcgdata/geneseq/geneseqp/AA1983.DAT:*
- 5: /SID58/gcgdata/geneseq/geneseqp/AA1984.DAT:*
- 6: /SID58/gcgdata/geneseq/geneseqp/AA1985.DAT:*
- 7: /SID58/gcgdata/geneseq/geneseqp/AA1986.DAT:*
- 8: /SID58/gcgdata/geneseq/geneseqp/AA1987.DAT:*
- 9: /SID58/gcgdata/geneseq/geneseqp/AA1988.DAT:*
- 10: /SID58/gcgdata/geneseq/geneseqp/AA1989.DAT:*
- 11: /SID58/gcgdata/geneseq/geneseqp/AA1990.DAT:*
- 12: /SID58/gcgdata/geneseq/geneseqp/AA1991.DAT:*
- 13: /SID58/gcgdata/geneseq/geneseqp/AA1992.DAT:*
- 14: /SID58/gcgdata/geneseq/geneseqp/AA1993.DAT:*
- 15: /SID58/gcgdata/geneseq/geneseqp/AA1994.DAT:*
- 16: /SID58/gcgdata/geneseq/geneseqp/AA1995.DAT:*
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- 18: /SID58/gcgdata/geneseq/geneseqp/AA1997.DAT:*
- 19: /SID58/gcgdata/geneseq/geneseqp/AA1998.DAT:*
- 20: /SID58/gcgdata/geneseq/geneseqp/AA1999.DAT:*
- 21: /SID58/gcgdata/geneseq/geneseqp/AA2000.DAT:*
- 22: /SID58/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2042	100.0	394	21	AAV79674
2	2042	100.0	394	21	AAV87291
3	1819	89.1	405	21	AAV95230
4	1116	54.7	374	21	AAV18807
5	1116	54.7	374	21	AAV18813
6	773	37.9	408	22	AAV1804
7	379	18.6	361	22	AAV31805
8	369	18.1	370	20	AAV30648
9	369	18.1	411	20	AAV28497
10	363	17.8	411	20	AAV34133
11	363	17.8	411	20	AAV28496

12	363	17.8	411	22	AAV50044	Human TREK. Homo
13	329.5	16.1	393	21	AAV94425	Human h-TREK poly
14	329.5	16.1	393	21	AAV94426	Human h-TREK poly
15	326.5	16.0	398	20	AAV30647	A mechanically sen
16	320.5	15.7	336	18	AAV23397	Twik-1 potassium c
17	320.5	15.7	336	21	AAV9673	Human potassium ch
18	319	15.6	499	21	AAV90356	Human TWIK-2 prote
19	319	15.6	499	21	AAV79675	Human potassium ch
20	319	15.6	499	21	AAV94875	Human protein clon
21	295.5	14.5	313	20	AAV34132	Human potassium ch
22	295.5	14.5	313	20	AAV25116	Human hTREK-1 prot
23	295.5	14.5	313	21	AAV90355	Human TWIK-4 prote
24	295.5	14.5	313	21	AAV68737	K14, a TWIK family
25	295.5	14.5	313	21	AAV68738	Human TWIK-3 prote
26	294.5	14.4	332	21	AAV90354	Human TWIK-3 prote
27	278.5	13.6	995	17	AAV31799	Amino acid sequenc
28	253	12.4	336	17	AAV97966	F22b7.7 potassium
29	245.5	12.0	395	22	AAV31801	Amino acid sequenc
30	231.5	11.3	618	17	AAV97984	DMOR1 potassium c
31	212.5	10.4	730	22	AAV31800	Amino acid sequenc
32	190.5	9.3	383	21	AAV9677	Caenorhabditis ele
33	176.5	8.6	107	20	AAV28498	Partial h-TREK1 po
34	156.5	7.7	1153	22	AAV31802	Amino acid sequenc
35	156	7.6	347	21	AAV9676	Caenorhabditis ele
36	151	7.4	316	21	AAV4160	Arabidopsis thalia
37	151	7.4	316	21	AAV40370	Arabidopsis thalia
38	151	7.4	408	21	AAV4159	Arabidopsis thalia
39	151	7.4	408	21	AAV40369	Arabidopsis thalia
40	147.5	7.2	132	22	AAV31803	Amino acid sequenc
41	141	6.9	128	21	AAV40248	Human ORFX ORF12 p
42	141	6.9	399	21	AAV41831	Arabidopsis thalia
43	141	6.9	424	21	AAV41830	Arabidopsis thalia
44	141	6.9	436	21	AAV41829	Arabidopsis thalia
45	131.5	6.4	646	20	AAV34123	Human potassium ch

ALIGNMENTS

RESULT 1	AAV79674	AAV79674
ID	AAV79674	standard; Protein: 394 AA.
XX	AAV79674:	
AC		
XX		
DT	29-AUG-2000	(first entry)
XX		
DE	Human potassium channel TASK1.	
XX		
KW	TASK1; TWIK-related acid-sensitive K+ chan	human;
KW	potassium channel; drug screening; hyperten	
KW	hypotensive; epilepsy; arrhythmia; vascular	ases;
KW	neurodegenerative disease; ischaemia; anoxia;	ndocrine disease;
KW	muscle disease; therapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	53
FT	Modified-site	/note= "N-glycosylated"
FT	Modified-site	323
FT	Modified-site	/note= "O-phosphorylated"
FT	Modified-site	383
FT	Modified-site	/note= "O-phosphorylated"
FT	Modified-site	392
FT	Modified-site	/note= "O-phosphorylated"
FT	Modified-site	393
XX	/note= "O-phosphorylated"	
XX		
XX	WO200027871-A2.	
XX		
XX	18-MAY-2000.	
XX		

PF 09-NOV-1999; 99MO-IB01886.
 XX
 PR 09-NOV-1998; 98US-0107692.
 PR 08-NOV-1999; 99US-0436265.
 PA
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Duprat F, Lesage F, Lazdunski M;
 DR WPI: 2000-376487/32.
 DR N-PSDB; AAA27746.
 XX
 PT New nucleic acid encoding a non-inactivating outwardly rectifying
 PT potassium transport channel, designated TASK2, useful in the treatment
 PT of hypertension or dysfunctions of the kidney, liver or pancreas -
 XX
 PS Disclosure; Fig 8; 91pp; English.
 XX
 CC The present sequence is that of human TASK1 (TWIK-related
 CC acid-sensitive K⁺ channel), a member of a new family of 2P
 CC domain potassium channels, also including TWIK-1 (see AAY79673) and
 CC novel TASK2 (see AAY79675). TASK1 is expressed in many different
 CC tissues, and at particularly high levels in pancreas and placenta.
 CC Host cells expressing TWIK-1 family members can be used to screen
 CC for substances that modulate the activity of members of the TWIK-1
 CC family of potassium channels. The drugs identified may be
 CC useful in the treatment of diseases of the heart or of the nervous
 CC system, such as epilepsy, arrhythmia, vascular diseases,
 CC neurodegenerative diseases, kidney, liver or pancreas diseases,
 CC hypertension, diseases associated with ischaemia or anoxia,
 CC endocrine diseases associated with anomalies of hormone secretion,
 CC and muscle diseases.
 CC
 XX
 XX Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;
 Best Local Similarity 100.0%; Pred. No. 4.2e-214;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MKRQNVLTALIVCTFTYLLVGAANFPALESEPELIERORLEKQELRARINISGGYE 60
 |||||||
 QY 61 ELERVLRLPHKAGVOMRFAGSEFYATVITTTGYGAAPSTDGKVFQCFYALLGIP 120
 |||||||
 DB 61 elervlrlphkagvwmrfagsfyaitvitttgygaapstdgkvyfcmfyllgip 120
 |||||||
 QY 121 TLVWFOSLGERINTLVRLYLRHAKKGLGMRRADYSMMANWVIGFSCISTLCIGAAAF 180
 |||||||
 DB 121 tlwvfogslgerintlvryllrhakkglgmrradysmmanwvligfscistlcigaaaf 180
 |||||||
 QY 181 YEHTFPQAYVYCFITLTGFGDYVALQMDAONQPOVAASEFYVILTGITATGAF 240
 |||||||
 DB 181 yehwtfqayyctfittgfygvalqkdqalqtpyvaistfyllgltvigafln 240
 |||||||
 QY 241 LVVLFRTMAEDERKDAERHALLTRNGOAGGGGSAHTTDDPAASSTAAGGGGFNNV 300
 |||||||
 DB 241 lvvlftrtmaedekraehalltrngagggggsahttdpaasstaagggfnnv 300
 |||||||
 QY 301 AEVLHFOQSMCSLMWYKREKLQVSIPIWIRPDUSTSPTCVQSHSSPGGGGRVSDPSSR 360
 |||||||
 DB 301 aevlhfoqsmcslmwkyrcklqvsiipiwirpdustsptcvqshsspggggrvsdpssr 360
 |||||||
 QY 361 CLCSGAPRSALISSYSTGLSLSTFRGIMKRSSV 394
 |||||||
 DB 361 clcsgaprsaisvstglslstfrgimkrssv 394

RESULT 2
 ID AAY87291
 ID AAY87291 standard; Protein: 394 AA.
 XX

AC AAY87291;
 XX
 XX 11-MAY-2000 (first entry)
 DE
 DE Human signal peptide containing protein HSP1-6; SEQ ID NO:68.
 KW Human: signal peptide containing protein; HSP1-6; diagnosis; cancer;
 KW inflammation; cardiovascular disease; antic; anti-inflammatory;
 KW antimicrobial; neuroprotective; anti; anti-inflammatory;
 KW antistimulant; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 XX MO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99MO-US14484.
 XX
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCY-) INCYTE PHARM INC.
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guebler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 DR WPI: 2000-160673/14.
 DR N-PSDB; AA298176.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 XX
 XX Claim 1; Page 207-208; 327pp; English.
 XX
 CC AA298109 to AA298242 encode AAY87224 to AAY87277 which represent the
 CC human signal peptide-containing proteins HSP1-6 to HSP1-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, corticotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). They are used to diagnose, or
 CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSP
 CC from natural sources.
 XX
 XX Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;

QY 181 YEHWFQAYVYCFITLTITGFGDYVALOKDQLOTPQVAFSFIITLGLVIGAFIN 240
 DB 181 ceewstfhayycifltitltitgdyvalokdqlkpklyvafstfmylvgltvigafln 240
 QY 241 LVVLFRTMAAEDEKRDARALTRNGAGGGGSAHTTPTASTAAGGGGFENY 300
 DB 241 lvvlfirtmasederdaeraasl-----agrrnsmvlihepepps-----rpy 286
 QY 301 -AEVLHFOQSCIMYKSRKQLQYIPMIIPRLSTSDTCVEOSHSSPGCGRYSDTPSR 359
 DB 287 kadvpdlqsvscctcyrsq---ygrsvapqnsfsaklaphfhsiskieispstlk 343
 QY 360 RCLCSGAPRAISVSSTGLHSLSTFRLGMRKRSV 394
 DB 344 nsifp---spissispglshfchqrlmkrrksv 374
 RESULT 6
 AAB31804 ID AAB31804 standard; Protein; 408 AA.
 AC AAB31804;
 XX 15-MAY-2001 (first entry)
 DT Amino acid sequence of a TWIK7 polypeptide.
 DE
 XX Tandem pore domain weak inward potassium protein: TWIK; TWIK2; TWIK3;
 KM TWIK4; TWIK5; TWIK6; TWIK7; TWIK1; pesticide; ion channel.
 OS Drosophila melanogaster.
 XX
 XX Key Location/Qualifiers
 FH 9..25
 FT Domain /note= "transmembrane domain 1"
 FT 78..101 /note= "Pore domain"
 FT 109..125 /note= "transmembrane domain 2"
 FT 161..177 /note= "transmembrane domain 3"
 FT 184..207 /note= "transmembrane domain 4"
 FT Domain /note= "pore domain"
 FT 224..240 /note= "transmembrane domain 4"
 XX
 PN MO200109301-A2.
 PD 08-FEB-2001.
 XX 27-JUL-2000; 2000MO-US20439.
 PF 28-JUL-1999; 99US-0362842.
 PR (GENO-) GENOPTERA LLC.
 PA Francis-Lang HL, Gillett LA, Margolis JS, Reddy BP, Winslow JM;
 PI Luo Y, Gendreau SB, Jacobus DA, Tietjen K, Nauen R, Jeschke P;
 XX WPI, 2001-159864/16.
 DR N-PSDB; AAF25380.
 XX
 XX New tandem pore domain weak inward rectifying potassium ion (TWIK)
 PT channel nucleic acids and proteins, useful in assays for identifying
 PT candidate compounds which are potential pesticides or therapeutics.
 XX
 PS Claim 5; Page 83-85; 96pp; English.
 CC The present sequence represents tandem pore domain weak inward potassium
 CC (K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4,
 CC TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and
 CC proteins are used in screening assays to identify candidate compounds
 CC which are potential pesticides or therapeutics. The TWIK channel nucleic

CC acids can be used for generating mutant ph
 CC in living cells that can be used to study
 CC regulation, and their use as pesticide or
 CC hybridisation probes and replication/amplic
 CC channel proteins are useful as immunogens
 CC polyclonal antibodies, and in assays to
 CC specifically bind to them. Genetically eng
 CC animals may be used in studying TWIK chan
 CC and identifying new drug targets, therapeut
 CC prognosis useful in treating disorders assoc
 XX
 SQ Sequence 408 AA:
 Query Match 37.9%; Score 773; Df
 Best local Similarity 43.6%; Pred. No. 1.3
 Matches 164; Conservative 66; Mismatches
 QY 1 MKRONVFTALIVCTFTYLLVGAIVEDALESEPELLER 306ELRARNVLSGGYE 60
 DB 1 mkkqnvrtllivctfyllivgaavfdaleselekrrv 3aedmlkkynisgedfk 60
 QY 61 ELERVYLRLKPKHAGVQMRAGSEFYAITVITITGV 306ELRARNVLSGGYE 60
 DB 61 vmetvylkseshkagqwkltgaltgaltvltltgy 3aedmlkkynisgedfk 60
 QY 121 TLVWFOSLGRINTLVYLLHRAKKGGMRADVSMA 306ELRARNVLSGGYE 60
 DB 121 glvmfsgigervrnllsylvkavrsrlckrtvasew 3aedmlkkynisgedfk 60
 QY 179 SHYEHWFQAYVYCFITLTITGFGDYVALOKDQAL 306ELRARNVLSGGYE 60
 DB 179 sklegwydsyvcifltitltitgdyvalqrdnalor 3aedmlkkynisgedfk 60
 QY 239 LNLVYLRFTMAAEDEKRDARALTRNGAGGGGSAHTTPTASTAAGGGGFENY 306ELRARNVLSGGYE 60
 DB 239 lnlvlrtfvmnteder-eaagmqalgyavklegda 3aedmlkkynisgedfk 60
 QY 286 SSTAAAGGGGFRNVYAEVLHFOQSCIMYKSRKQLQYIPMIIPRLSTSDTCVEOSHSSPGCGRYSDTPSR 306ELRARNVLSGGYE 60
 DB 298 -----nissmschclngnrth 3aedmlkkynisgedfk 60
 QY 321 -LQYSIPMIIP-RDLS 334
 DB 339 hlrhlpevymqdl 354
 RESULT 7
 AAB31805 ID AAB31805 standard; Protein; 361 AA.
 AC AAB31805;
 XX 15-MAY-2001 (first entry)
 DT Amino acid sequence of a cpb-TWIK1 polypept
 DE
 XX Tandem pore domain weak inward potassium pr
 KM TWIK4; TWIK5; TWIK6; TWIK7; TWIK1; pesticide
 OS Leptinotarsa decemlineata.
 XX
 XX Key Location/Qualifiers
 FH 46..60
 FT Domain /note= "transmembrane doma
 FT 125..149 /note= "Pore domain"
 FT 156..176 /note= "transmembrane doma
 FT 204..231 /note= "transmembrane doma
 FT 235..259 /note= "pore domain"
 FT Domain /note= "pore domain"
 CC in animal models or
 CC channels, their
 CC targets, and as
 CC primers. TWIK
 CC create monoclonal or
 CC molecules that would
 CC metazoan invertebrate
 CC ability, and for screening
 CC agents, diagnostics and
 CC with ion channels.

FT	Domain	274..296	/note="transmembrane domain 4"
XX			
PN	WD200109301-A2.		
PD	08-FEB-2001.		
XX			
PF	27-JUL-2000; 2000MO-US20439.		
XX			
PR	28-JUL-1999; 99US-0362842.		
XX			
PA	(GENO-) GENOPTERA LLC.		
PI	Francis-Lang HL, Gillett LA, Margolis JS, Reddy BP, Winslow JW;		
PI	Luo Y, Gendreau SB, Jacobus DA, Tietjen K, Nauen R, Jeschke P;		
XX	WPI: 2001-159864/16.		
DR	N-PSDB: AAF25381.		
XX			
XX			
FT	New tandem pore domain weak inward rectifying potassium ion (TWIK)		
PT	channel nucleic acids and proteins, useful in assays for identifying		
XX	candidate compounds which are potential pesticides or therapeutics -		
XX			
PS	Claim 5; Page 87-88; 96pp; English.		
XX			
CC	The present sequence represents tandem pore domain weak inward potassium		
CC	(K ⁺) (TWIK) polypeptide. The specification describes TWIK, TWIK3, TWIK4		
CC	TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and		
CC	proteins are used in screening assays to identify candidate compounds		
CC	which are potential pesticides or therapeutics. The TWIK channel nucleic		
CC	acids can be used for generating mutant phenotypes in animal models or		
CC	in living cells that can be used to study the ion channels, their		
CC	regulation, and their use as pesticide or drug targets, and as		
CC	hybridisation probes and replication/amplification primers. TWIK		
CC	channel proteins are useful as immunogens to generate monoclonal or		
CC	polyclonal antibodies, and in assays to identify molecules that would		
CC	specifically bind to them. Genetically engineered metazoan invertebrate		
CC	animals may be used in studying TWIK channel activity, and for screening		
CC	and identifying new drug targets, therapeutic agents, diagnostics and		
CC	prognosis useful in treating disorders associated with ion channels.		
XX			
XX			
Sequence	361 AA;		

```

Query Match          18.6%; Score 379; DB 22; Length 361;
Best Local Similarity 32.4%; Pred. No. 1e-32;
Matches 110; Conservative 52; Mismatches 113; Indels 64; Gaps 13

OY 1 MKRQVRLTLLVCVFYTLVGAAPFDALSEPELLERQLEROE-LRARNLSGGY 59
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 39 mektfifslsyfayfmficsgaafsyfeapeealrvklglavagkflvsnprvdaql 98
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 60 EELERVNLRLKPKHKGAV-----QWRFGSFYEATVTTTIGYGAAPSTDCGXVF 109
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 99 eel--lvelvtrannrgvasalenatsepnmsfgsfstavlvtllygvtpstirngkflf 156
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 110 CMEVALGLGPIELVMEQSGERINFLVRLRLRAKKGLD-----MRADVSNAMWVLI 162
   ||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 157 cmfkyavagvplclvllsalverlllprtvallqwlmsklqhlpyqrltrvhlaiylvll 216
   ||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 163 GPFSCISTFLCIGAAAFSHYE-HWTFQOAYVYCFITLTGGFYVALQKDOALOT-QPOY 220
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 217 vff-----llpraafaslepewdyldslylfcistltlgldyL--pgdsahqpyrvpi 269
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 221 VAFSEVYILTLGTLVGAFINLV-----DREMTMAEDEKRDAAEHALLTRNGOAGG 272
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 270 klmctcyflfgltlm-mtlctlvfdipqlnlgllfttbedsek-----vllasgpp 319
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 273 G---GGGSAHTTDTAASSTAAAGGGFRNVVAEVLHFQS 308
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 320 glqygaqfagfshned-----nlhqvrvrvrs 344

```

[illegible]

QY 217 QPOYVAFSEVYILGLTVIGAFNLV--VLEFMTMAEDEKRD-AEHRALLTRN 267
 Db 267 Idfykpvvfwlvglayfaavismigdwlrviskkckeeygetrahaewtan 320

RESULT 9

AAI28497
 ID AAY28497 standard; Protein; 411 AA.

XX AAY28497;

XX 12-OCT-1999 (first entry)

XX Mouse h-TREK1 polypeptide.

XX h-TREK1: two pore potassium channel; inflammatory disease;
 KM chromosome 1q32.

OS Mus musculus.

PN MO9937762-A1.

XX 29-JUL-1999.

XX 02-DEC-1998; 98MO-EP07805.

XX 09-OCT-1998; 98GB-0022135.

XX 27-JAN-1998; 98EP-0300570.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Chapman CG, Meadows HJ;

XX WPI: 1999-469126/39.

XX N-PSDB; AA200040.

XX New two pore potassium channel used for, e.g. treatment of cancer,
 PT pulmonary, cardiovascular and inflammatory diseases

XX Claim 3; Page 26; 44pp; English.

XX This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1
 CC polynucleotide AA200040. h-TREK1 is a two pore potassium channel.

CC The polynucleotide sequence of h-TREK1 can be used to diagnose a
 CC disease or susceptibility to a disease related to expression or activity
 CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the

CC treatment of diseases including cancer, pulmonary, cardiovascular, and
 CC inflammatory diseases, pain, psychiatric disorders including depression
 CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
 CC stroke, and head trauma and neurological disorders including migraine.

XX Sequence 411 AA;

SO

Query Match 18.1%; Score 369; DB 20; Length 411;

Best Local Similarity 31.6%; Pred. No. 1.5e-31;

Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRONVTLLALVCTFFYLLVGAAPDALSEPLLRORLENOELRARNYLSGGYE 60

Db 42 mkwktvstflfv--vylilgaavfkaleqpgisqrltvlqkqfllaqhacvns--t 97

QY 61 ELEENVRL-KPRKAGV-----OMRFAGSEFYATVTITIGYNAAPSTDGKY 108

Db 98 eldeliqvvaahaglipgnssngvshwdlgsstffagvtlclfgnlsprteggk 157

QY 109 FCFMYALGIPLLVMOQSLGERINTLVRYLLHRAKGLGNRRAD-----VSM 156

Db 158 fccllyallgplpflgllagvgdqltlf-----gkglakvedcfikwnvsqtklri 208

QY 157 ANMWLIFPSCISTLTCGAAAFSHYEWTFQOAYVYCFITLTITGFGDYALAKDQALQT 216

Db 209 lslilifgcglvalpavlfkhiegwsaldalyfv--lfgfdyvggsd--ley 266
 QY 217 QPOYVAFSEVYILGLTVIGAFNLV--VLEFMTMAEDEKRD-AEHRALLTRN 267
 Db 267 Idfykpvvfwlvglayfaavismigdwlrviskkckeeygetrahaewtan 320

RESULT 10

AAI28497
 ID AAY34133 standard; Protein; 411 AA.

XX AAY34133;

XX 30-NOV-1999 (first entry)

XX Human potassium channel K-Hnov59.

XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 KM cardiovascular disorder; CNS disorder; renal disorder.

OS Homo sapiens.

PN MO9943696-A1.

XX 02-SEP-1999.

XX 22-FEB-1999; 99MO-US03826.

XX 19-JAN-1999; 99US-0116448.

XX 25-FEB-1998; 98US-0076687.

XX 07-AUG-1998; 98US-0095836.

XX (AXYS-) AXYS PHARM INC.

XX Curran ME, Hu P, Miller AP, Rutter M, et al;

XX WPI: 1999-527591/44.

XX N-PSDB; AA211915.

XX New nucleic acids encoding mammalian K-Hnov proteins, useful for the diagnosis and treatment of episodic ataxia
 PT with myokymia, cardiac arrhythmia, epilepsy, and Bartter's syndrome

XX Claim 3; Page 104-105; 112pp; English.

XX This sequence represents the human K-Hnov59 potassium channel.

CC K-Hnov proteins have a high degree of homology to known potassium
 CC channels and may be alpha subunits, which form the functional channel,
 CC or accessory subunits that act to modulate channel activity. K-Hnov59
 CC is a 4 transmembrane domain, 2 pore domain potassium channel. The gene
 CC is located on chromosome 19, determined via chromosome

CC localization using primers AA211919 and AA211920. K-Hnov cDNAs
 CC were isolated by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple

CC independent clones. Potassium channels have critical roles in various
 CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia;

CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.

CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS)

CC disorders. Nucleotides encoding K-Hnov proteins may be used for
 CC identifying homologous or related proteins and the DNA sequences encoding
 CC them. They may be used to produce compositions that modulate the

CC expression and function of the K-Hnov protein and in studying the
 CC biochemical pathways associated with it. They may also be used for the

CC recombinant production of K-Hnov protein in transfection cultures.

CC Additionally, such nucleotides may be used to design therapy protocols for
 CC the treatment of diseases associated with abnormal potassium channels.

XX Sequence 411 AA;

SO

Query Match	17.8%; Score 363; Dh	Length 411;
Best Local Similarity 31.0%; Pred. No. 7e-3		
Matches 91; Conservative 59; Mismatches		Indels 42; Gaps
1 MKRKNVETLALICTFTYLLVGAAPDALESEPELIER	1 RROELRARNYLSOGYE 60	
42 mkktvsttliv--vlylllgatvkaaleqphelsqr	14qqtllsqscvsn--t 97	
61 ELERVVLR-L-KPKKACV-----QWRPAGSFVY	11TTIGYGHAAPSTDGKV 108	
98 eldelldqivaainagvllplgntsqhswldgssffl	11tligfmsptleggkl 157	
109 FCMFVYALGLPFLVWFOSLGERINTLVYLLHRKKGL	1RAD-----VSM 156	
158 fcllyallglplglfllagvgdqlgtlfl-----	1kvedtlfkwnvsqtklri 208	
157 ANNVLGFECISITLCIGAAFSHEHWTFPOAYVYCF	1TIGFGDYVALORDALOT 216	
209 istclifllfgcvlfvalpalrlfkhegwsaladyfvr	11tfgdyvavgsd--ley 266	
217 QPQYVAFSEVYIITGLTVIGAPLNLV--VLRPMNNAE	1D-AERPALITRN 267	
267 ldfykpvvfwfmlvglyafavlsimgdlwlriskkl	11ghrahaewtan 320	
RESULT 12		
AAB50044		
ID AAB50044 standard; Protein; 411 AA.		
AC AAB50044;		
DE 19-MAR-2001 (first entry)		
XX Human TREK.		
XX Human; TREK; 2p domain potassium channel; 1.6 ng membrane potential; 1.6 ng modulation; epilepsy; 1.6 ng neurological disorder; sleep-related disorder; attention deficit disorder; addiction; anxiety; Parkinson's chorea; Huntington's chorea; cerebellar dysfunction; alopecia.		
XX Homo sapiens.		
XX W0200072863-A2.		
XX 07-DEC-2000.		
XX 01-JUN-2000; 2000WO-GB02107.		
XX 01-JUN-1999; 99GB-0012733.		
XX (SMK) SMITHKLINE BEECHAM PLC.		
XX Hervieu GJ, Meadows HJ, Randall AD;		
XX WPI; 2001-080422/09.		
XX N-PDB; AAC90412.		
XX use of human TREK1 polypeptide, polynucleotides of h-TREK1 polypeptides for treating disorders, addiction and dyskinesias including Huntington's chorea -		encoding them and epilepsy, sleep-related Parkinson's and
XX Claim 7; Page 29; 35pp; English.		
XX The present sequence is human TREK1 (h-TREK1) which play a part in the control of resting membrane potential. Modulation of these channels will therefore affect neuronal excitability, the leading to a modulation		

XX MPI: 2000-365583/31.
 DR N-PSDB: AAA27106.
 XX
 PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel
 PT family of polypeptides, useful for the diagnosis and treatment of
 PT h-TRAAK related disorders, e.g. depression and schizophrenia
 XX
 PS Claim 12: Pages 21 and 22; 35pp: English.
 XX
 CC Functional genomics was used to identify h-TRAAK polypeptides and
 CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK
 CC polypeptides have homology to the 2P domain potassium channel family of
 CC polypeptides. The h-TRAAK polypeptides and polynucleotides may
 CC be used in diagnostic assays for conditions related to h-TRAAK
 CC imbalance and for identifying agonists and antagonists of h-TRAAK
 CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also
 CC be useful for treatment and prevention (e.g. as vaccines) of certain
 CC diseases, such as pain, psychiatric disorders including depression and
 CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke
 CC and head trauma and neurological disorders including migraine and
 CC epilepsy. The present sequence is human h-TRAAK protein #2.
 CC
 XX
 SQ Sequence 393 AA:

Query Match 16.1%; Score 329.5; DB 21; Length 393;
 Best Local Similarity 31.0%; Pred. No. 2,9e-27;

Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;

OY 9 LALIVCTFTYLLVGAAPFALSEPEP-LIERORLELRODELARVNLNQ----- 56
 DB 7 Lallalvlllylvgalvfgaleqhegqgqrelgevrekltahpcvsdqlillkeva 66
 OY 57 ---GVEELERVVLRKPKRAGVOMRPAFSFYATVITTTIGGHAAPSDGKVCMEY 113
 DB 67 dalggagpelpsstnsnsa---wldgsaffsgfllitllygnvalitdgrllclly 123
 OY 114 ALLGIPLTVMFQSLGERINTLVRYLLHRAKGLGMRAD-----VSMANVLLIG 163
 DB 124 alvgiprlflllagvdrigrsslrh-----gihleaifllkwyppelavrlsamfll 176
 OY 164 FFSCTSTLCIGAAAFSHYEHMTFFQAYVYCFTLTITIGEDVVALQKDALQTOPQYVAF 223
 DB 177 lhgcllfvlrptfvcymedwskleaylfvyltlvsgfyagadpr--qdsplayqr 234
 OY 224 SFVYITLTC-----LTVIGAFNLVLRMTNADDERDAHRALLTRNGAGGGGG 276
 DB 235 vwflllglayfasvltlignwlvrvsr-----traemgltltaqa 275
 OY 277 GSAHTTDTASSSTAAG 292
 DB 276 aswtgvtarvcgrag 291

RESULT 15

AA30647
 ID AAY30647 standard: Protein; 398 AA.

XX AAY30647;

XX 18-NOV-1999 (first entry)

DE A mechanically sensitive potassium channel protein TRAAK.

XX Mechanically sensitive potassium channel protein; TRAAK;
 KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
 KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
 KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
 KW muscular disease.

XX Mus sp.

OS

XX

PN WO9945108-A2.

PD 10-SEP-1999.

XX 23-FEB-1999; 99WO-FR00404.

XX 05-MAR-1998; 98FR-0002725.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Honore E, Fink M, Lazdunski M, Lesage F, et al F;

XX MPI: 1999-551038/46.

XX N-PSDB: AA210606.

PT New mechanically sensitive potassium channel used to screen for
 PT specific modulators, potential therapeutic drugs for heart and nervous
 PT system disorders

PS Claim 2: Fig 1: 40pp: French.

CC The present sequence represents a mechanical sensitive potassium
 CC channel protein designated TRAAK. The protein is activated by
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by
 CC riluzole. The protein is used to screen for specific modulators which
 CC are useful for treating or preventing diseases of the heart and nervous
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
 CC (arrhythmia), neurodegeneration (particular Alzheimer's disease),
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular
 CC disease. The protein itself may be used to detect it in tissues,
 CC antibodies specific for the protein are used to detect it in tissues,
 CC also as therapeutic inhibitors or activators.

SQ Sequence 398 AA:

Query Match 16.0%; Score 326.5; DB 21; Length 398;
 Best Local Similarity 31.5%; Pred. No. 6.4e-27;

Matches 85; Conservative 45; Mismatches 112; Indels 45; Gaps 7;

OY 9 LALIVCTFTYLLVGAAPFALSEPEP-LIERORLELRODELARVNLNQ----- 67
 DB 7 Lallalvlllylvgalvfgaleqhegqgqkmdhgrd-----dpvsgksledflliv 66
 OY 68 RLKPKRAGVQ-----WRFAGSFYFATVITTTIGGHAAPSDGKVCMEYVAL 115
 DB 67 ealggagpelpsstnsnsaawlglsaffsgfllitllygnvalitdgrllclly 126
 OY 116 LGIPLTVMFQSLGERINTLVRYLLHRAKGLGMRAD-----DVSANVLLIG 162
 DB 127 vglpflgmlllagvdrigrsslr-----rgihleaifllkwyppelavrlsamfll 179
 OY 163 GFSCTSTLCIGAAAFSHYEHMTFFQAYVYCFTLTITIGEDVVALQKDALQTOPQYVAF 220
 DB 180 g---cllfvlrptfvcymedwskleaylfvyltlvsgfyagadpr--qdsplayqr 234
 OY 221 -----VAFSFVYITLTCIGAFNLVLRMTNADDERDAHRALLTRNGAGGGGG 245
 DB 235 lvwflllglayfasvltlignwlvrvsr-----traemgltltaqa 275

Search completed: August 28, 2001, 17:05:48
 Job time: 1893 sec

[Illegible text]

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:06:22 ; Search time 28.01 Seconds

(without alignments)
289,632 Million cell updates/sec

Title: US-09-503-089a-5

Perfect score: 2042
Sequence: 1 MKRONVRLALIVCTFTYLL.....STGLHSLSTFRLKMKRRSSV 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5a_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5b_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6a_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6b_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCOTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	18.1	411	4	US-09-236-080-6
2	363	17.8	411	4	US-09-236-080-2
3	320.5	15.7	336	3	US-08-749-816-2
4	253	12.4	336	1	US-08-332-312-4
5	231.5	11.3	618	1	US-08-332-312-2
6	190.5	9.3	383	3	US-08-749-816-4
7	176.5	8.6	107	4	US-09-236-080-4
8	156	7.6	347	3	US-08-749-816-3
9	103	5.0	532	1	US-08-288-405A-10
10	102.5	5.0	626	2	US-08-956-242-2
11	102.5	5.0	626	3	US-09-351-215-2
12	99.5	4.9	494	1	US-08-464-340A-4
13	99.5	4.9	494	5	PCR-US94-08449A-4
14	99.5	4.9	888	3	US-08-956-242-4
15	99.5	4.9	888	3	US-09-351-215-4
16	97	4.8	255	2	US-09-342-084-11
17	97	4.6	1159	2	US-08-956-242-13
18	94	4.6	1159	3	US-09-351-215-13
19	94	4.6	1159	4	US-09-226-012-2
20	94	4.6	1159	4	US-09-226-012-4
21	92.5	4.5	233	4	US-09-342-084-12
22	90.5	4.4	407	2	US-08-742-440A-3
23	90.5	4.4	509	2	US-09-031-392-6
24	90.5	4.4	509	4	US-09-299-549-6
25	88	4.3	376	1	US-08-614-801A-6
26	87	4.3	528	2	US-08-527-152-2
27	85	4.2	27	3	US-08-749-816-5

28	85	4.2	27	3	US-08-749-816-6	Sequence 6, Appl1
29	84.5	4.1	281	4	US-09-053-702-2	Sequence 2, Appl1
30	84	4.1	1239	2	US-08-937-931-2	Sequence 2, Appl1
31	84	4.1	1239	4	US-09-285-502-2	Sequence 2, Appl1
32	81	4.0	553	4	US-09-083-351-2	Sequence 2, Appl1
33	81	4.0	553	4	US-09-083-352-2	Sequence 2, Appl1
34	80	3.9	242	2	US-08-553-497A-2	Sequence 26, Appl1
35	80	3.9	242	2	US-08-553-497A-2	Sequence 26, Appl1
36	80	3.9	488	1	US-08-553-497A-2	Sequence 22, Appl1
37	80	3.9	488	1	US-08-115-365-2	Sequence 2, Appl1
38	80	3.9	488	1	US-08-586-897-2	Sequence 2, Appl1
39	79.5	3.9	270	2	US-08-652-507-2	Sequence 2, Appl1
40	79.5	3.9	817	2	US-08-820-170A-2	Sequence 28, Appl1
41	79.5	3.9	817	3	US-09-055-699-28	Sequence 28, Appl1
42	79.5	3.9	817	4	US-09-273-565-28	Sequence 28, Appl1
43	79.5	3.9	829	2	US-08-820-170A-31	Sequence 31, Appl1
44	79.5	3.9	829	3	US-09-055-699-31	Sequence 31, Appl1
45	79.5	3.9	829	4	US-09-273-565-31	Sequence 31, Appl1

ALIGNMENTS

RESULT 1
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217e1 Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match	18.1%	Score 369	DB 4	Length 411
Best local Similarity	31.6%	Pred. No. 1.6e-12		
Matches	93	Conservative	57	Mismatches 102; Indels 42; Gaps 9
OY	1	MKRONVRLALIVCTFTYLLVGAIVDALESEPELLERORL:RODELARYLISGGYE 60		
DB	42	MKRWVSTTFLLV--VLVLIGAIVKALEOPEISQRTIVIOKOTFLAHCVNS--T 97		
OY	61	ELERVVLRL-KPHKAGV-----QWRFAFSFYPAIT-ITTFGHAAPSTDGKV 108		
DB	98	ELDELIOQVIAINACIITPLGNSNOYSHMDGSSFFFGCTVTTTGGFNVAGSGKI 157		
OY	109	PCMFVALLGIPITLVFOSLGERINTLVRYLHRAKGLGMRAD-----VSM 156		
DB	158	FCITVALLGIPLEFGLAGVGDQDGTIF-----GCIKAVEDTFTKMNVSQTKIRI 208		
OY	157	ANNVILGFSCISTLCIGAAPSHEWTFPOAYYYCFITITIGGDVVALOKDALOT 216		
DB	209	ISTITIFLFCGVLFVLPVIFKHIGWSALDAIYFV--TTIGGDVAVAGSD--IEY 266		
OY	217	QPOYVAFSFPVILITGLVIGAFNLV--VLRFPTNMAI--ID-AEHRALLTRN 267		
DB	267	LDFYKRVWFWILVGLAYPAVALISMIGDLRVISKTK--JEFRHAHAEMTAN 320		
RESULT 2				
US-09-236-080-2				
; Sequence 2, Application US/09236080				
; Patent No. 6242217				
; GENERAL INFORMATION:				

RESULT 4
 US-08-332-312-4
 Sequence 4, Application US/08332312
 Patent No. 5559026
 GENERAL INFORMATION:
 APPLICANT: Price, Laura A.
 APPLICANT: Pausch, Mark H.
 TITLE OF INVENTION: Functional Expression
 TITLE OF INVENTION: Melanagaster Putative
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07470-8426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,312
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Harrington, James J.
 REGISTRATION NUMBER: .P-38,711
 REFERENCE/DOCKET NUMBER: 32,421
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-831-3246
 TELEFAX: 201-831-3305

Query match 11.38; Score 231.5; DB 1; Length 618;

```

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 383 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-4

Query Match 9.3%; Score 190.5; DB 3; Length 383;
Best Local Similarity 24.0%; Pred. No. 9.8e-13;
Matches 62; Conservative 48; Mismatches 95; Indels 53; Gaps 9;

QY 11 LIVCTFYLLVGAVALDALESEPELIERQRLERQELRARY--NLQSG--GYEELE-- 63
DB 44 LVLSCTVYALGAYLVFLSIHPELKRREKRAIREPDLKQGFMGNTSGIENSQSIET 103
QY 64 --RVVLRK-PHKAQV-----QWRPAGSFYFAITVITTTGCHAAPSTDGK 107
DB 104 TKKLILMLEDAHNAHAEYEFNLHHEIPKDMWTFSSALVFTTTVIVPGYGFVSAVGR 163
QY 108 VFCMEYALLGIPPLVWFQSLGERINTLVRYLLHRAKKGIGMRADVSMANV----- 160
DB 164 MCLINALALGIPPLVMTADTGKFAOLV-----TRWFGDNMMALPAALFVCLLPAYP 216
QY 161 -LIGFSCISTLCIGAAAFSHYEHMTFFQAYYVCFITLTITIGFDYVALQDQALQTOPQ 219
DB 217 LVVGEILCSTS-----NITFLDSVFSLSITIFIGFD--LTPDMNVHML 261
QY 220 YVAFSPVYITGTIVICA 237
DB 262 FLAVGVLTITDIYVA 279

RESULT 7
US-09-236-080-4
Sequence 4, Application US/09236080
Patent No. 6242217
GENERAL INFORMATION:
APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-080-4

Query Match 8.6%; Score 176.5; DB 4; Length 107;
Best Local Similarity 33.0%; Pred. No. 5e-12;
Matches 34; Conservative 22; Mismatches 26; Indels 21; Gaps 2;
QY 78 WRPAGSFYFAITVITTTGCHAAPSTDGKVFQMFALLGIPPLVWFQSLGERINTLV 137
DB 9 WDLGSSFFFGAGVITTTGFGNISPRTEGKIFCIYALGIPPLFGLLAGVGDQLGTF- 67
QY 138 YLLHRAKKGIGMRAD-----VSMANVILGFSFI 168
DB 68 -----GKGIKAVEDTFIKMNVSQTKIRIISTITIFILGCV 102

RESULT 8
US-08-749-816-3
Sequence 3, Application US/08749816
Patent No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemaire, Eric

APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunki, Michel
APPLICANT: Romey, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patentin Release #1.0, Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8394
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-3

Query Match 7.6%; Score 156; DB 3; Length 347;
Best Local Similarity 22.6%; Pred. No. 5.7e-05;
Matches 52; Conservative 45; Mismatches 6; Indels 36; Gaps 6;

QY 3 RQNVRLALIVCTFTYL--LVGAVALDALESEPELIERQRLERQELRARYNLSQGY 59
DB 31 RQNVVAVVCSAATILVFNLAGIFLYAETQ--SSSES; NENSEVSKLHNPIG- 86
QY 60 EELERVVLRKPH-----KAGVQWFPAGSEFYFAITVITTTI VGHAA PSTDGKVCMEY 113
DB 87 -----KITAEKSKLKGCLTKRSKIDGFGKAIFFSWLYSVAGSLYPSHTLGRYITTY 142
QY 114 ALGIPPLVWFQSLGERINTLVRYLLHRAKKGIGMRADVSMAN----- 158
DB 143 SLTIMIPVFIKFEFGTFLAHFLVAVSNRTR--LAVKAVYKLSQBPENAEPPSNLSQHD 200
QY 159 --WVLGFSICISTLCIGAAAFSHYEHMTFFQAYYVCFITLTITIGFDV 206
DB 201 YLFLSSLLCISLSSSALFSSISNISVLSVYGGITMFLIGIDIV 250

RESULT 9
US-08-288-405A-10
Sequence 10, Application US/08288405A
Patent No. 5559009
GENERAL INFORMATION:
APPLICANT: Chandu, Kantalathara G.
APPLICANT: Kaiman, Katalin
APPLICANT: Chandu, Grischu
APPLICANT: Gutman, George A.
TITLE OF INVENTION: A No. 5559009el Voltage-gated Potassium Channel

TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert,
ATTORNEY: Altn: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,405A
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,431
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-59844-1/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-405A-10

Query Match 5.0%; Score 103; DB 1; Length 532;
Best Local Similarity 22.8%; Pred. No. 0.0085;
Matches 34; Conservative 27; Mismatches 36; Indels 52; Gaps 7;

OY 3 RQNVETLALIVCTFTYLLVGAAPDALESEPELLERORLELROELRARNYLSOGGYEEL 62
DB 382 RASMEELGILT---SELPIGVLFSS-----AVY-----FAEV 411
OY 63 ERVVLRLKPKHAGVQWRPAGSEFYFAITVTTTIGYGHAAPOSTDGKVFCEMFAVALLGI 118
DB 412 DRV---DTHFTSI---PESEFMVAIVMTTGVGDMAPVTVGKIVGSLAIAVLFTIS 463
OY 119 -PLTIVMOSLGERINTLVRYLILHRAKKG 146
DB 464 LPVPVIV-----SNFSYFYHRETEG 483

RESULT 10
US-08-956-242-2
Sequence 2, Application US/08956242C
GENERAL INFORMATION:
PATENT NO. 5986081
APPLICANT: Ganetzky, Barry S.
TITLE OF INVENTION: Polynucleotides Encoding Herg-3
FILE REFERENCE: 960296.94550
CURRENT APPLICATION NUMBER: US/08/956,242C
CURRENT FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Homo sapien

FEATURE:
NAME/KEY: unsure
LOCATION: (441)..(542)
OTHER INFORMATION: unidentified at time of filing
US-08-956-242-2

Query Match 5.0%; Score 102.5; DB 2; Length 626;
Best Local Similarity 23.7%; Pred. No. 0.012;
Matches 33; Conservative 32; Mismatches 4; Indels 29; Gaps 5;

OY 9 LALIVCTFTYLLVGAAPDALESEPELLERORLELROELRARNYLSOGGYE 60
DB 274 LFLMCTFALLAHMLACIMVAIGN---VERPYLEHRTGK---SLAVOLGKRYNGSD--- 325
OY 61 ELERVVLRLKPKHAGVQWRPAGSEFYFAITVTTTIGYGHAAPOSTDGKVFCEMFAVALLGI 120
DB 326 -----PASGPSVQOKYVYALYFTFSSILTSVGFVNV---SNFNSKEVFSICVMLIG--- 373
OY 121 TLVMPQSLGERINTLVRYL 139
DB 374 -SLMVASIFGNVSATIORTL 391

RESULT 11
US-09-351-215-2
Sequence 2, Application US/09351215
PATENT NO. 6087468
GENERAL INFORMATION:
APPLICANT: Ganetzky, Barry S.
TITLE OF INVENTION: Polynucleotides Encoding Herg 3
FILE REFERENCE: 960296.94550
CURRENT APPLICATION NUMBER: US/09/351,215
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 08/956,242
EARLIER FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: unsure
LOCATION: (441)..(542)
OTHER INFORMATION: unidentified at time of filing
US-09-351-215-2

Query Match 5.0%; Score 102.5; DB 4; Length 626;
Best Local Similarity 23.7%; Pred. No. 0.012;
Matches 33; Conservative 32; Mismatches 4; Indels 29; Gaps 5;

OY 9 LALIVCTFTYLLVGAAPDALESEPELLERORLELROELRARNYLSOGGYE 60
DB 274 LFLMCTFALLAHMLACIMVAIGN---VERPYLEHRTGK---SLAVOLGKRYNGSD--- 325
OY 61 ELERVVLRLKPKHAGVQWRPAGSEFYFAITVTTTIGYGHAAPOSTDGKVFCEMFAVALLGI 120
DB 326 -----PASGPSVQOKYVYALYFTFSSILTSVGFVNV---SNFNSKEVFSICVMLIG--- 373
OY 121 TLVMPQSLGERINTLVRYL 139
DB 374 -SLMVASIFGNVSATIORTL 391

RESULT 12
US-08-464-340A-4
Sequence 4, Application US/08464340A
PATENT NO. 5710019
GENERAL INFORMATION:
APPLICANT: LI, ET AL.

```

1 TITLE OF INVENTION: Human Potasssium Channel 1 and 2 Proteins
2 NUMBER OF SEQUENCES: 13
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
5 ADDRESSEE: CECCHI, STEWART & OLSTEIN
6 STREET: 6 BECKER FARM ROAD
7 CITY: ROSELAND
8 STATE: NEW JERSEY
9 COUNTRY: USA
10 ZIP: 07068
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: 3.5 INCH DISKETTE
13 COMPUTER: IBM PS/2
14 OPERATING SYSTEM: MS-DOS
15 SOFTWARE: WORD PERFECT 5.1
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/464,340A
18 FILING DATE: June 5, 1995
19 CLASSIFICATION: 435
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: PCT/US94/08449
22 FILING DATE: 28 JUL 1994
23 ATTORNEY/AGENT INFORMATION:
24 NAME: FERRARO, GREGORY D.
25 REGISTRATION NUMBER: 36,134
26 REFERENCE/DOCKET NUMBER: 325800-415
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 201-994-1700
29 TELEFAX: 201-994-1744
30 INFORMATION FOR SEQ ID NO: 4:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 494 AMINO ACIDS
33 TYPE: AMINO ACID
34 STRANDEDNESS:
35 TOPOLOGY: LINEAR
36 MOLECULE TYPE: PROTEIN
37 US-08-464-340A-4

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1 TITLE OF INVENTION: Potassium Channel Protein I and 2
2
3 NUMBER OF SEQUENCES: 4
4 CORRESPONDENCE ADDRESSES:
5 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
6 ADDRESSEE: CECCHI, STEWART & OLSTEIN
7 STREET: 6 BECKER FARM ROAD
8 CITY: ROSELAND
9 STATE: NEW JERSEY
10
11 COUNTRY: USA
12 ZIP: 07068
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: 3.5 INCH DISKETTE
16
17 COMPUTER: IBM PS/2
18 OPERATING SYSTEM: MS-DOS
19 SOFTWARE: WORD PERFECT 5.1
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: PCT/US94/08449A
22 FILING DATE: SUBMITTED HEREWITH
23
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28
29 ATTORNEY/AGENT INFORMATION:
30 NAME: FERRARO, GREGORY D.
31 REGISTRATION NUMBER: 36,134
32 REFERENCE/DOCKET NUMBER: 325800-105
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 201-994-1700
35 TELEFAX: 201-994-1744
36
37 INFORMATION FOR SEQ ID NO: 4:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 494 AMINO ACIDS
40 TYPE: AMINO ACID
41 STRANDEDNESS:
42 TOPOLOGY: LINEAR
43
44 MOLECULE TYPE: PROTEIN
45
46 PCT-US94-08449A-4

APPLICANT:	Ganetzky, Barry S.
APPLICANT:	Titus, Steven A.
TITLE OF INVENTION:	Polynucleotides Encoding Herg-3
FILE REFERENCE:	960296.94550
CURRENT APPLICATION NUMBER:	US/08/956,242C
CURRENT FILING DATE:	1997-10-22
NUMBER OF SEQ. ID NOS:	13
SOFTWARE:	PatentIn Ver. 2.0
SEQ. ID NO. 4	
LENGTH:	888
TYPE:	PRT
ORGANISM:	Homo sapien
FEATURE:	
NAME/KEY:	unsure
LOCATION:	(113)
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY:	unsure
LOCATION:	(438)
OTHER INFORMATION:	Unidentified at time of filing
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NAME/KEY:	unsure
LOCATION:	(439)
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY:	unsure
LOCATION:	(567)
OTHER INFORMATION:	Unidentified at time of filing
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NAME/KEY:	unsure
LOCATION:	(568)
OTHER INFORMATION:	Unidentified at time of filing
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NAME/KEY:	unsure
LOCATION:	(571)
OTHER INFORMATION:	Unidentified at time of filing
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NAME/KEY:	unsure
LOCATION:	(575)
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY:	unsure
LOCATION:	(580)
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NAME/KEY:	unsure
LOCATION:	(589)
OTHER INFORMATION:	Unidentified at time of filing
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NAME/KEY:	unsure
LOCATION:	(593)
OTHER INFORMATION:	Unidentified at time of filing
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NAME/KEY:	unsure
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OTHER INFORMATION:	Unidentified at time of filing
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NAME/KEY:	unsure
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NAME/KEY:	unsure
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NAME/KEY:	unsure
LOCATION:	(610)
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	

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1 NAME/KEY : unsure
2 LOCATION : (611)
3 OTHER INFORMATION: Unidentified at time of filling
4 FEATURE:
5 NAME/KEY : unsure
6 LOCATION : (621)
7 OTHER INFORMATION: Unidentified at time of filling
8 FEATURE:
9 NAME/KEY : unsure
10 LOCATION : (624)
11 OTHER INFORMATION: Unidentified at time of filling
12 FEATURE:
13 NAME/KEY : unsure
14 LOCATION : (625)
15 OTHER INFORMATION: Unidentified at time of filling
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17 NAME/KEY : unsure
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19 OTHER INFORMATION: Unidentified at time of filling
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41 NAME/KEY : unsure
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46 LOCATION : (661)
47 OTHER INFORMATION: Unidentified at time of filling
48 FEATURE:
49 NAME/KEY : unsure
50 LOCATION : (662)
51 OTHER INFORMATION: Unidentified at time of filling
52 US-08-956-242-4
53
54 Query Match 4.9%; Score 99.5; DB: 2; Length 888;
55 Best Local Similarity 19.5%; Pred. No. 0.045
56 Matches 31; Conservative 34; Mismatches 18; Indels 49; Gaps
57
58 Oy 46 OELRARNVNSGGYELEENVLRLPKHKGVMRFAGSYFVATVTTTGYGHAAPSTDG 105
59 Db 236 OQIGRRYNDSDS-----SGPSIDKVTALITFSSILTSVGFNVSPNTNS 282
60 Oy 106 GNFCMFYALGIPPLVWFOSLGRINPLVYL-----LHRAKKG 146
61 Db 283 EKIFISICWLGIS---SLMYASIFGVSAIIIRLVSCTA--AKOMLRVKEPIRFHQIPMP 338
62 Oy 147 LGMRRAD-----VSANMVLIGFSCIT-STLCI 173
63 Db 339 LRORLEEFVHAMVYTNGLDM-NMVLKGFPECLQADICL 338

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RESULT	15
US-09-351-215-4	
Sequence 4, Application US/09351215	
Patent No. 6087488	
GENERAL INFORMATION:	
APPLICANT: Ganetzky, Barry S.	
APPLICANT: Titus, Steven A.	
TITLE OF INVENTION: Polynucleotides Encoding Herg-	
FILE REFERENCE: 960296.94550	
CURRENT APPLICATION NUMBER: US/09/351,215	
CURRENT FILING DATE: 1999-07-12	
EARLIER APPLICATION NUMBER: 08/956,242	
EARLIER FILING DATE: 1997-10-22	
NUMBER OF SEQ ID NOS: 13	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 4	
LENGTH: 888	
TYPE: PRT	
ORGANISM: Homo sapien	
FEATURE:	
NAME/KEY: unsure	
LOCATION: (133)	
OTHER INFORMATION: Unidentified at time of filing	
FEATURE:	
NAME/KEY: unsure	
LOCATION: (181)	
OTHER INFORMATION: Unidentified at time of filing	
FEATURE:	
NAME/KEY: unsure	
LOCATION: (438)	
OTHER INFORMATION: Unidentified at time of filing	
FEATURE:	
NAME/KEY: unsure	
LOCATION: (439)	
OTHER INFORMATION: Unidentified at time of filing	
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NAME/KEY: unsure	
LOCATION: (567)	
OTHER INFORMATION: Unidentified at time of filing	
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NAME/KEY: unsure	
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OTHER INFORMATION: Unidentified at time of filing	
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NAME/KEY: unsure	
LOCATION: (599)	
OTHER INFORMATION: Unidentified at time of filing	
FEATURE:	
NAME/KEY: unsure	
LOCATION: (600)	
OTHER INFORMATION: Unidentified at time of filing	

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	Query Match	4.9%	Score 99.5	Dp 37	Length 888
	Best Local Similarity	19.58%	Pred. No. 0.04%		
	Matches 31	Conservative 34	Mismatches 45	Indels 49	Gaps 6
0y	46	CELRRYNSGGGEELEERVVRLKPKRAGVWRFGAS	*-A	VITTTGCGHAPSTDG	105

Db 236 QQIGKRYNDSDS-----SGPSIKDYVTAALYFTFSSLTSVGFQNVSPNTNS 282
QY 106 GKVCMEYALIGIPLTVMFQSLGERINTLVRYL-----LHRAKG 146
Db 283 EKFSICVMLIG---SLMVASIFGNVSAIQRLXSGTARYHOMLNKKEFIRRHQIPNP 338
QY 147 LGMRRAD-----VSMANNVLIGFESCI-STLCI 173
Db 339 LKORLEEFQHAMTYTNGIDM-NMYLKGPFECLOADICL 376

Search completed: August 28, 2001, 17:06:23
Job time: 527 sec

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R:Muray, J.; Wohldmann, P.; O'Neal, D.

Submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid F34D6.

A:Reference number: Z21153

A:Accession: T32347

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-336 <MUR>

A:Cross-references: EMBL:AF025454; PIDN:AC71151.1; GSPDB:GN00020; CESP:F34D6.3

A:Experimental source: strain Bristol N2; clone F34D6

C:Genetics:

A:Gene: twk-23; CESP:F34D6.3

A:Map position: 2

A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match

Best Local Similarity 39.5%; Score 806.5; DB 2; Length 336;

Matches 172; Conservative 54; Mismatches 84; Indels 53; Gaps 8;

1 MKRONVTLALIVCTFTYLLVGAAPDALESEPELLR-----KORLELRQDELARAYN 53

1 MKRONVTLALIVCTFTYLLVGAAPDALESEPELLR-----KORLELRQDELARAYN 60

54 LSQGYEELERVVLRKPKRAGVQWRFAGSFYFAITVITTTIGYGAAPSTDCGKFCMFY 113

61 MSNADYILLETATYKSVPHKAGVQWRFAGSFYFAITVITTTIGYGAAPSTDCGKFCMFY 120

114 ALGIPPLTVFOSLGRINTLVRYLLHRKAKGLGMRADVSMANVLLGFCSTLTCT 173

121 ALADIPPLGLMFOSIGGRMTFAKLRFRIRAG-KQPIVTSDDLIT--FCTGMCGLLI 177

174 -GAASRSHHEHMTFFOAYYCFITLTFTIGFDVALOKOALOTOPQYAFSPVYLLTG 231

178 FCGAFMSSSTENTMTFPAAYVYCFITLTFTIGFDVALOKOALOTOPQYAFSPVYLLTG 237

232 LTVIGAFNLVLRKMTMAEDEKRADEHRL-----LTRNGOAGGGGGSAHTTDTASS 287

238 LTVISAMNLLVLRFLMTNTEREDERDEALIAAGLVRFVGDPTADDFGLPLSDNVSL 297

288 TAAAGGGGFRNVVAEVLHFOSSCMLTKSKREKQYISIPMIIPDLSTSDTCVQSHSSP 347

298 AS-----CSC-YQLPDEKLRH-----HRKHTEP 320

348 GGG 350

321 HGG 323

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4 ONVETLALIVCTFTYLLVGAAPDALESEPELLR-----KORLELRQDELARAYN 63

7 KSARALLILSTFTYLLFGAMVFDKLESEKDTWVRDEIF--TRKHKYVFSERDLHFE 66

64 RVLRLKPKRAGVQWRFAGSFYFAITVITTTIGYGAAPSTDCGKFCMFY 123

67 AIAIKSIPQOAGVQWRFAGSFYFAITVITTTIGYGAAPSTDCGKFCMFY 126

124 MFSIGGRINTLVRYLLHRKAKGLGMR-----RADVSMANVLLGFCSTLTCT 175

127 MFSIGGRINTLVRYLLHRKAKGLGMR-----RADVSMANVLLGFCSTLTCT 182

176 AARSHEHMTFFOAYYCFITLTFTIGFDVALOKOALOTOPQYAFSPVYLLTG 235

183 YMFHTTEKMSIFDPAAYVYCFITLTFTIGFDVALOKOALOTOPQYAFSPVYLLTG 242

236 GAEFLNLVLRKMTMAEDEKRADEHRL-----LTRNGOAGGGGGSAHTTDTASS 287

243 SACCNNLLVLRKMTMAEDEKRADEHRL-----LTRNGOAGGGGGSAHTTDTASS 297

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Page 2

A:Accession: S65566; MUID:96183184
A:Reference number: S65566;
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: EMBL:U33632; NID:q1086490; PIDD:AAB01668.1; PID:q1086491

Query Match	15.78;	Score 320.5;	DB 2;	Length 336;
Best Local Similarity	32.48;	Pred. No. 1.5e+21;		
Matches	90;	Conservative	47;	Mismatches 102;
				Indels 39;
				Gaps 9;

[illegible]

RESULT 6
T28933
hypothetical protein C52B9.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #extl-change 18-Feb-2000
C:Accession: T28933
R:Nelson, J.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C52B9.
A:Reference number: Z20545
A:Accession: T28933
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-513 <NGL>
A:Cross-references: EMBL:U64596; PIDN:AAC47976.1; GSPDB:GN00028; CESP:C52B9.6
A:Experimental source: strain Bristol NZ; clone C52B9
C:Genetics:
A:Gene: CESP:C52B9.6
A:Map position: X
A:Introns: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 452/3

[illegible]

```

Db 232 SKKITISQVRSQSSQSSRSSSSVMQSSKAGSMNMDHIDSDSEF-----DELRIPEVNVLLVLLAY- 260
QY 166 SCISITLCIGAAAFSFIHEHMTFFQAYVYCITLITIGFST-----LLOKQDALQTOPOYVAFSF 225
Db 291 -----TALGGFLFQSWHELEFEEAFYFCETLMAVVGFC-----PNEOYVAFETM 337
QY 226 VYILGTGLVIAEAFNLV-----VLRFMTNNAEDKEKDA-----ALTRNCOAGGGGGGSA 279
Db 338 AVIIFGGLSLAMCIDLNGSTVIRIKIHVLGFMEDAK-----GAVMVGSLQNGEH 365
QY 260 HTTDTASSTAAAGGGGFRNNVYAEVLHRO-----SMCSCLN-----SHEKLOTISLPM----- 327
Db 366 LKHHGTIEVITAGGKLVQVGAALSSREARELOMSYVL-----YQHRNVLEPPLGNLAKV 445
QY 328 -----IIPDLSTSDPCVQSSHS 345
Db 446 VKENAIKILPDIITEKQYIVQNS 470

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RESULT 7
 T25392
 hypothetical protein T28A8.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
 C:Accession: T25392
 R:Lloyd, C.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z20027
 A:Accession: T25392
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <WIL>
 A:Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSDB:GN00021; CESP:T28A8.1
 A:Experimental source: clone T28A8
 C:Genetics:
 A:Gene: CESP:T28A8.1
 A:Map position: 3
 A:Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/1; 464/2

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Query Match      14.3% Score 293; DP: 67; Length 393;
Best Local Similarity 26.6%; Pred. No. Ge-1;
Matches 78; Conservative 57; Mismatches 96; Indels 62; Gaps 9.

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RESULT 8
T23907
hypothetical protein R04F11.4 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C/Accession: T23907
R/Harris, B.
submitted to the EMBL data library, June 1996

A:Reference number: Z19816
 A:Accession: T23907
 A>Status: preliminary; translated from GB/EMBL/DBDB
 A:Molecule type: DNA
 A:Residues: 1-524 <MIL>
 A:Cross-references: EMBL:Z74475; PIDN:CAA98957.1; GSPDB:GN00023; CESP:F04F11.4
 A:Experimental source: clone R04F11
 C:Genetics:
 A:Gene: CESP:R04F11.4
 A:Map position: 5
 A:Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2

Query Match 13.5%; Score 275; DB 2; Length 524;
 Best Local Similarity 23.9%; Pred. No. 3.8e-17;
 Matches 88; Conservative 38; Mismatches 92; Indels 150; Gaps 9;

QY 11 LIVCTFTYLLVGAADFALDESEPELERORLEKQOELRARY-----52
 DB 18 LVLLISGYTLGALCFHNYEKRYEQQLRNETSRIGELKRNVDQLRMSNGTASTWR 77
 QY 53 NLGGGVEELERVY-----RLKPH-----KAGVORFAGSFPAITVITTTIGYGAAP 101
 DB 78 QTADGMDLELRDVFMDYTRNYMPDDVIYGDGPDKMSFSLFSPWATATTIGYGHIVP 137
 QY 102 STDGKVFCEFYALLGIPFLVMEFOSLGERINTLV-----136
 DB 138 RTDEGRVAIIFFYALGLGIPFLVITADIGRFLATYIIKLHGYAMVMSFVNSCLKIKMA 197
 QY 137 -----RY-----LHRAKK-----GLGMR-----150
 DB 198 CCMVRLRRRIIMPTELLQRTOKLYPNNNPVAATAASAGSGTGRKKQQRDNVSDAG 257
 QY 151 -----RADVSMAMVLIIGFSCSTICIG 174
 DB 258 TFDNISINDSGEGENEGEEEOIQDPDSNEKRVSVLEFILLMLGY-----VAGG 311
 QY 175 AAASFYEHNTFFQAYYYCFTTLTTIGFQYVALQKDAOTOPQYVAFSFTVLTGLTV 234
 DB 312 AYIYRMWEMWTFEAFYFCFVTVTTIGFQDIVPANVD-----WLPATLAYIVFGLII 363
 QY 235 IGAFLNLY 242
 DB 364 TTMCIDLV 371

RESULT 9

T30037
 hypothetical protein F20A1.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T30037
 R:Gating, S.; Wu, X.
 submitted to the EMBL Data Library, March 1996
 A:Description: The sequence of C. elegans cosmid F20A1.
 A:Reference number: Z20726
 A:Accession: T30037
 A>Status: preliminary; translated from GB/EMBL/DBDB
 A:Molecule type: DNA
 A:Residues: 1-1539 <GAT>
 A:Cross-references: EMBL:U053150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F20A1.7
 A:Experimental source: strain Bristol N2; clone F20A1
 C:Genetics:
 A:Gene: CESP:F20A1.7
 A:Map position: 5
 A:Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110

Query Match 13.1%; Score 268; DB 2; Length 1539;
 Best Local Similarity 24.6%; Pred. No. 6.2e-16;
 Matches 96; Conservative 60; Mismatches 126; Indels 108; Gaps 13;
 QY 8 TLALIVCTFTYLLVGAADFALDESEPELERORLEKQOELRA-RYNLSGGG 58

DB 88 TPKLLIITIGLYSFGIAHIFNYLEVLPDLEAREDFHQRIKINLVMLNLALFIYDNRNEDR 147
 QY 59 YEELERVVLRKAKHKAGVQ-----WRFAGSFYFAITVITIGYGAAPSTDGKVFCEM 111
 DB 148 EEMKRAHILKFE-EDIGLEPEVIEIETWTFMMSFLYAGTII-IGYNIACKTRAGOTATM 206
 QY 112 FYALLGIPFLVMEFOSL-----132
 DB 207 VYAFVGIPMLVMTLSINNFLKMIKLITNGVSDMTLYTC-AGIVYRDEVOKRLRT 266
 QY 133 ---NTLVRYLL--HRAKKGMRADVSMANM-----VLIGFSCISTL 171
 DB 267 KLAKTMRKRLSKHGAPSSIAISNSEENRLNSPDEDI-CHODPPVSLTIATVAMI 326
 QY 172 CIGAAAFSHENHTFFQAYYYCFTTLTTIGFQYVALV-MAOTOPQYVAFSFTVILTIG 231
 DB 327 ILSAAVFCLEFEDWTFEFSFCEISLTITIGLD-----VTPANDEVIAATFGVVIYG 378
 QY 232 LTVYGAFLNLVLRFMVMAEDEKRDHAERALLTRNCG-AGGGGSAHTTDTASTAA 291
 DB 379 LSLITVCTIDVLOEKLAOMY-----ALLQKLEIYEM-DRNAASAMA 425
 QY 292 GGGG-----FRNYAEVL-HFQSMCS 311
 DB 426 GFGGAKFELMPLLSKNEGAKVMDFKODCS 455

RESULT 10

T21598
 hypothetical protein F31D4.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21598
 R:Kortliffe, B.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z19447
 A:Accession: T21598
 A>Status: preliminary; translated from GB/EMBL/DBDB
 A:Molecule type: DNA
 A:Residues: 1-443 <MIL>
 A:Cross-references: EMBL:Z92832; PIDN:CAB07375.1; GSPDB:GN00023; CESP:F31D4.7
 A:Experimental source: clone F31D4
 C:Genetics:
 A:Gene: CESP:F31D4.7
 A:Map position: 5
 A:Introns: 13/3; 90/2; 149/1; 222/3; 290/3

Query Match 12.8%; Score 262; DB 2; Length 443;
 Best Local Similarity 25.0%; Pred. No. 4.7e-16;
 Matches 78; Conservative 55; Mismatches 113; Indels 66; Gaps 9;

QY 11 LIVCTFTYLLVGAADFALDESEPELERORLEKQOELRARNLSQ-----56
 DB 17 LIIVFLYICISGLHVEFLIEPYQELRDAMQHKIENNRFARVDAMKKIFNNSDYLIYI 76
 QY 57 -----CGYELEERVVLRKPKHAGVORFAGSFPAITVITTTIGYGAAP 100
 DB 77 KGMTSORLTTFTFIEELGSYEN---QIGVAKWSQOKMDWVWNLVAGTCTTIGYGHY 132
 QY 101 PSTDGVKVFCEFYALLGIPFLVMEFOSLGERINTLVYI-LHFAKKGL-----147
 DB 133 PMTDAGMLTMRITALRCIPMLLVLDQFGLLITTKMFYFQIKRLMRRIMRCTQPIE 192
 QY 148 -----GMRADVSMANVLI-IGFSCISTPLCIGAAAFSHYEH-WTFQAYYYCFTTLTT 199
 DB 193 EMKEIEROERHDDIDFLPPLPGIALIVTWIFICSFVLSVNDHNMWLTLESFYFFTSIST 252
 QY 200 IGFQDYVALQKDAOTOPQYVAFSFTVILTGLTVIGN-ANVLRPMT---ANADEKR 256
 DB 253 VGLGDIV-----PSSPRLITMFGFILLVGLSVSN-ILNLOAKRKSTVEAGRDEKT 304

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:13:14 ; Search time 21.03 Seconds

(without alignments)
641.781 Million cell updates/sec

Title: US-09-503-089a-5

Sequence: 1 MKRQVRLTALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	ID	Description
1	204.2	100.0	394	CIW3_HUMAN	014649 homo sapien
2	1850.5	90.6	411	CIW3_RAT	054912 ratius norv
3	1840.5	90.1	409	CIW3_MOUSE	035111 mus musculu
4	370	18.1	411	CIW2_MOUSE	P97438 mus musculu
5	364	17.8	426	CIW2_HUMAN	095069 homo sapien
6	329.5	16.1	393	CIW4_HUMAN	088454 mus sapien
7	326.5	16.0	398	CIW4_MOUSE	088454 mus musculu
8	320.5	15.7	336	CIW1_HUMAN	090180 homo sapien
9	319	15.6	499	CIW5_HUMAN	095279 homo sapien
10	318.5	15.6	336	CIW1_MOUSE	008581 mus musculu
11	295.5	14.5	313	CIW6_HUMAN	095257 homo sapien
12	261.5	12.8	1001	ORK1_DROME	094526 dtrosophila
13	259.5	12.7	335	TRK8_CAEEL	P34410 caenorhabdi
14	224	11.0	307	CIW7_HUMAN	093242 homo sapien
15	221	10.8	307	CIW8_MOUSE	093242 mus musculu
16	170	8.3	691	TKO1_YEAST	P40310 saccharomyc
17	112.5	5.5	490	CIK1_DROME	062246 dtrosophila
18	99.5	4.9	1174	CIKE_DROME	062246 dtrosophila
19	98	4.8	1743	TAGC_DICDI	Q33866 dictyosteli
20	97.5	4.8	228	CIW1_MOUSE	010937 caenorhabdi
21	97.5	4.8	432	AZAR_LABOS	091081 labrus ossi
22	96.5	4.7	449	IFR1_MOUSE	P19182 mus musculu
23	94.5	4.6	209	Y139_MERJA	057603 methanococc
24	94.5	4.6	385	PER_DROME	P16686 dtrosophila
25	94.5	4.6	449	IFR1_RAT	P20693 ratius norv
26	94.5	4.6	647	KNRL_DROME	P13054 dtrosophila
27	94	4.6	262	VG38_BPT2	P07875 bacterioph
28	94	4.6	287	WC2A_ARATH	P33266 arabidopsia
29	94	4.6	1159	HERG_HUMAN	Q12809 homo sapien
30	93.5	4.6	285	WC2C_ARATH	P30302 arabidopsia
31	93	4.6	529	CIK6_HUMAN	P17658 homo sapien
32	93	4.6	602	CIK5_RAT	P19024 ratius norv
33	92.5	4.5	653	CIK4_HUMAN	P22459 homo sapien

34	92.5	4.5	655	CIK4_RAT	P15385 ratius norv
35	92	4.5	451	IFR1_HUMAN	O00458 homo sapien
36	92	4.5	598	CIK5_RABIT	P05638 oryctolagus
37	91.5	4.5	660	CIK4_BOVIN	O05037 bos taurus
38	91.5	4.5	1581	WGLP-BEV	P23052 berne vitus
39	91	4.5	601	CIK5_MOUSE	P79197 mustela put
40	90.5	4.4	290	LEP4_PSEAE	P22610 pseudomonas
41	90.5	4.4	369	PAR3_MOUSE	O08675 mus musculu
42	90.5	4.4	509	GTR4_HUMAN	P14672 homo sapien
43	90.5	4.4	654	CIK4_MOUSE	O28527 mustela put
44	90	4.4	393	IRK9_HUMAN	Q92806 homo sapien
45	90	4.4	499	CIK2_HUMAN	P16389 homo sapien

ALIGNMENTS

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RESULT 1
ID      CIW3_HUMAN      STANDARD:      PRT: 394 AA.
AC      014649:
DT      01-OCT-2000 (Rel. 40, Created)
DT      01-OCT-2000 (Rel. 40, Last sequence update:
DE      POTASSIUM CHANNEL, SUBFAMILY K MEMBER 3 (AC
DE      CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-S
GN      KCNK3 OR TASK.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Ve
OC      Mammalia; Eutheria; Primates; Catarrhini; P
OX      NCBI_Taxid=9606;
[1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=99254548; PubMed=10321245;
RA      Duprat F., Lesage F., Fink M., Reyes R., Hu
RT      TASK, a human background K+ channel to se
RT      near physiological pH.
RL      EMBO J. 16:5464-5471 (1997).
[2]
RN      [2]
RP      ACTIVATION.
RX      MEDLINE=99254548; PubMed=10321245;
RA      Patel A.J., Honore E., Lesage F., Fink M.,
RT      Inhalational anesthetics activate two-por
RT      channels.
RL      Nat. Neurosci. 2:422-426 (1999).
CC      -I- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENS
CC      CHANNEL PROTEIN. RECTIFICATION DIRECTI
CC      ION CONCENTRATION ON EITHER SIDE OF THE
CC      OUTWARD RECTIFIER WHEN EXTERNAL POTASSI
CC      WHEN EXTERNAL POTASSIUM CONCENTRATION
CC      -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRAN
CC      -I- TISSUE SPECIFICITY: WIDESPREAD EXPRESS
CC      EXPRESSION IN PANCREAS AND PLACENTA. L
CC      LUNG, PROSTATE, HEART, KIDNEY, UTERUS,
CC      -I- MISCELLANEOUS: INHIBITED BY EXTERNAL A
CC      HALOTHANE AND ISOFLURANE.
CC      -I- SIMILARITY: BELONGS TO THE TWO PORE DO
CC      CHANNELS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is
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CC      -----
CC      EMBL: AF006823; AAC51777.1;
CC      MIM: 603220;
CC      InterPro: IPR000099;
CC      InterPro: IPR001622;
CC      InterPro: IPR003092;

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DR InterPro: IPR003280; TWIK channel; 1.
 DR Pfam: PF02034; TASKCHANNEL.
 DR PRINTS: PR01095; TASKCHANNEL.
 DR PRINTS: PR01333; 2PORKCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 9 29 POTENTIAL.
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 108 128 POTENTIAL.
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 159 179 POTENTIAL.
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 223 243 POTENTIAL.
 FT DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 394 AA; 43518 MW; 9PFC8266F615FB7 CRC64;

Query Match 100.0%; Score 2042; DB 1; Length 394;
 Best Local Similarity 100.0%; Pred. No. 7, 3e-156;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALSEPELIERQLELRQDELARAYNLSGGYE 60
 1 MKRONVRLALIVCTFTYLLVGAAPDALSEPELIERQLELRQDELARAYNLSGGYE 60
 DB 1 MKRONVRLALIVCTFTYLLVGAAPDALSEPELIERQLELRQDELARAYNLSGGYE 60

QY 61 ELEENVRLRPHKAGVOMRFGSFYFAIVTTTGYHAAPSTGKVFCEMFAALLGIP 120
 61 ELEENVRLRPHKAGVOMRFGSFYFAIVTTTGYHAAPSTGKVFCEMFAALLGIP 120
 DB 61 ELEENVRLRPHKAGVOMRFGSFYFAIVTTTGYHAAPSTGKVFCEMFAALLGIP 120

QY 121 TLVWFOSLGERINTLVRYLLHRAKKGIMRRADYSMANMVLIGFSCISTLCIGAAAFSH 180
 121 TLVWFOSLGERINTLVRYLLHRAKKGIMRRADYSMANMVLIGFSCISTLCIGAAAFSH 180
 DB 121 TLVWFOSLGERINTLVRYLLHRAKKGIMRRADYSMANMVLIGFSCISTLCIGAAAFSH 180

QY 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240
 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240
 DB 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240

QY 241 LVVLRFTMAEDKRAEHRALLTRNGOAGGGGSAHTTDPASSAAAGGGGFRN 300
 241 LVVLRFTMAEDKRAEHRALLTRNGOAGGGGSAHTTDPASSAAAGGGGFRN 300
 DB 241 LVVLRFTMAEDKRAEHRALLTRNGOAGGGGSAHTTDPASSAAAGGGGFRN 300

QY 301 AEVLHFOSMSCIMYKSRKLYSIPMIIPRDLSTDCVQSHSSPGGGGYSDFPSR 360
 301 AEVLHFOSMSCIMYKSRKLYSIPMIIPRDLSTDCVQSHSSPGGGGYSDFPSR 360
 DB 301 AEVLHFOSMSCIMYKSRKLYSIPMIIPRDLSTDCVQSHSSPGGGGYSDFPSR 360

QY 361 CLCGAPRSALSSYSTGLHSLSTFRGLMKRRSSV 394
 361 CLCGAPRSALSSYSTGLHSLSTFRGLMKRRSSV 394
 DB 361 CLCGAPRSALSSYSTGLHSLSTFRGLMKRRSSV 394

RESULT 2
 C1W3_RAT STANDARD; PRT; 411 AA.
 ID C1W3_RAT
 AC 054912;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
 GN KNCX3 OR TASK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RX MEDLINE=8099797; Pubmed=9437008;
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
 RT "An open rectifier potassium channel with two pore domains in tandem

RT cloned from rat cerebellum.";
 RL J. Neurosci. 18:868-877(1998).
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW, WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART, MODERATE EXPRESSION IN LUNG AND BRAIN, LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.
 CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUPIVACAINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
 CC -----
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 CC -----
 CC EMBL: AF031384; AAC39952.1; -
 DR InterPro: IPR000099; -
 DR InterPro: IPR001622; -
 DR InterPro: IPR003092; -
 DR InterPro: IPR003280; -
 DR Pfam: PF02034; TWIK channel; 1.
 DR PRINTS: PR01095; TASKCHANNEL.
 DR PRINTS: PR01333; 2PORKCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 9 29 POTENTIAL.
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 108 128 POTENTIAL.
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 159 179 POTENTIAL.
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 223 243 POTENTIAL.
 FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 411 AA; 45276 MW; D277801609E215 CRC64;

Query Match 90.6%; Score 1850.5; DB 1; Length 411;
 Best Local Similarity 88.3%; Pred. No. 1, 5e-140;
 Matches 363; Conservative 8; Mismatches 2; Indels 17; Gaps 2;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALSEPELIERQLELRQDELARAYNLSGGYE 60
 1 MKRONVRLALIVCTFTYLLVGAAPDALSEPELIERQLELRQDELARAYNLSGGYE 60
 DB 1 MKRONVRLALIVCTFTYLLVGAAPDALSEPELIERQLELRQDELARAYNLSGGYE 60

QY 61 ELEENVRLRPHKAGVOMRFGSFYFAIVTTTGYHAAPSTGKVFCEMFAALLGIP 120
 61 ELEENVRLRPHKAGVOMRFGSFYFAIVTTTGYHAAPSTGKVFCEMFAALLGIP 120
 DB 61 ELEENVRLRPHKAGVOMRFGSFYFAIVTTTGYHAAPSTGKVFCEMFAALLGIP 120

QY 121 TLVWFOSLGERINTLVRYLLHRAKKGIMRRADYSMANMVLIGFSCISTLCIGAAAFSH 180
 121 TLVWFOSLGERINTLVRYLLHRAKKGIMRRADYSMANMVLIGFSCISTLCIGAAAFSH 180
 DB 121 TLVWFOSLGERINTLVRYLLHRAKKGIMRRADYSMANMVLIGFSCISTLCIGAAAFSH 180

QY 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240
 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240
 DB 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240

QY 241 LVVLRFTMAEDKRAEHRALLTRNGOAGGGGSAHTTDPASSAAAGGGGFRN 300
 241 LVVLRFTMAEDKRAEHRALLTRNGOAGGGGSAHTTDPASSAAAGGGGFRN 300
 DB 241 LVVLRFTMAEDKRAEHRALLTRNGOAGGGGSAHTTDPASSAAAGGGGFRN 300

QY 292 -----GGGGFRNVAEVLHFOSMSCIMYKSRKLYSIPMIIPRDLSTDCVQSHSSPGGGGYSDFPSR 343


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Db 301 GMYGVGSGGGRNYAEMLFQSMCSCLMYKSKNEKLYQSYIPILIPDLSTSTCEVHS 360
OY 344 HSPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 394
    ||||||| 361 HSPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 411
Db 361 HSPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 411

RESULT 3
C1W3_MOUSE STANDARD; PRT; 409 AA.
ID C1W3_MOUSE 035163;
AC 035163: 035163;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM
DE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL)
DE (CARDIAC TWO-PORE BACKGROUND K+ CHANNEL) (CTBAK-1).
GN KCNK3 OR TASK OR CTBAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98165556; PubMed=9506712;
RA Kim D., Fujita A., Horio Y., Kurechi Y.;
RT "Cloning and functional expression of a novel cardiac two-pore
RT background K+ channel (CTBAK-1).";
RL Circ. Res. 82:513-518(1998).
RN [2]
RP SEQUENCE OF 4-409 FROM N.A.
RX MEDLINE=97459933; PubMed=9312005;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations
RT near physiological pH.";
RL EMBO J. 16:5464-5471(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20287574; PubMed=10748056;
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT "Proton block and voltage gating are potassium-dependent in the
RT cardiac leak channel konk3.";
RL J. Biol. Chem. 275:16969-16978(2000).
CC -1- FUNCTION: PH-DEPENDENT VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
CC (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED
CC IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL
CC INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB008537; BAA25436.1; -
DR EMBL: AF006824; AAC53367.1; -
DR EMBL: AB013345; BAA28349.1; -
DR EMBL: AF241798; AAF81418.1; -
DR EMBL: AF242508; AAF81418.1; JOINED.

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DR MGD; MG1:1100509; Konk3.
DR InterPro: IPR000099; -
DR InterPro: IPR001622; -
DR InterPro: IPR003092; -
DR InterPro: IPR003280; -
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PRO1095; TASKCHANNEL.
DR PRINTS: PRO1333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 9 29 PORE-FORMING (POTENTIAL).
FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).
FT TRANSMEM 108 128 PORE-FORMING (POTENTIAL).
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 PORE-FORMING (POTENTIAL).
FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).
FT TRANSMEM 223 243 PORE-FORMING (POTENTIAL).
FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCN) (POTENTIAL).
FT CONFLICT 4 4 0 -> E (IM REP).
FT CONFLICT 123 123 V -> I (IN REP).
SQ SEQUENCE 409 AA; 45068 MM; 35236E011AAC; CRC64;

Query Match 90.1%; Score 1840.5; Length 409;
Best Local Similarity 88.5%; Pred. No. 9.2e-03;
Matches 362; Conservative 7; Mismatches 55; Indels 15; Gaps 2;

OY 1 MKRONVRLALIVCTFTYLLVGAALVDALESEPELIERC VROELRARNYNSGGYE 60
    ||||||| 1 MKRONVRLALIVCTFTYLLVGAALVDALESEPELIERC VROELRARNYNSGGYE 60
Db 1 MKRONVRLALIVCTFTYLLVGAALVDALESEPELIERC VROELRARNYNSGGYE 60
OY 61 ELERVVLRLKPKKGVQWRFSGFPFATVTTTGYGA STGGKVCMEFVALIGPL 120
    ||||||| 61 ELERVVLRLKPKKGVQWRFSGFPFATVTTTGYGA STGGKVCMEFVALIGPL 120
Db 61 ELERVVLRLKPKKGVQWRFSGFPFATVTTTGYGA STGGKVCMEFVALIGPL 120
OY 121 TLVNFOSIGERINTLVRLHRAKKGGLGMRADYSMAV TGFSCISTCIGNAAFSH 180
    ||||||| 121 TLVNFOSIGERINTLVRLHRAKKGGLGMRADYSMAV TGFSCISTCIGNAAFSH 180
Db 121 TLVNFOSIGERINTLVRLHRAKKGGLGMRADYSMAV TGFSCISTCIGNAAFSH 180
OY 181 YEHTFQAYVYCEITLTGTPGIDVALQKDALOTQCFASFVYLTGLVYIGAFIN 240
    ||||||| 181 YEHTFQAYVYCEITLTGTPGIDVALQKDALOTQCFASFVYLTGLVYIGAFIN 240
Db 181 YEHTFQAYVYCEITLTGTPGIDVALQKDALOTQCFASFVYLTGLVYIGAFIN 240
OY 241 LVVLRFTMNAEDKRDHRAALLTRNGOAGGGGSGSSATTTASTTAA- 291
    ||||||| 241 LVVLRFTMNAEDKRDHRAALLTRNGOAGGGGSGSSATTTASTTAA- 291
Db 241 LVVLRFTMNAEDKRDHRAALLTRNGOAGGGGSGSSATTTASTTAA- 291
OY 292 -----GGGGRNYAEEVLHFQSMCSCLMYKSKNEKLYQSYIPILIPDLSTSTCEVHS 345
    ||||||| 292 -----GGGGRNYAEEVLHFQSMCSCLMYKSKNEKLYQSYIPILIPDLSTSTCEVHS 345
Db 292 -----GGGGRNYAEEVLHFQSMCSCLMYKSKNEKLYQSYIPILIPDLSTSTCEVHS 345
OY 346 SPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 394
    ||||||| 346 SPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 394
Db 346 SPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 394
OY 361 SPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 411
    ||||||| 361 SPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 411
Db 361 SPGGGGRYSDTPSRRLCSGAPRASAISVSTGLHSLSTRGLMKRRSSV 411

RESULT 4
C1W2_MOUSE STANDARD; PRT; 411 AA.
ID C1W2_MOUSE 037438;
AC 037438:
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TASK) (TWO-PORE POTASSIUM CHANNEL TPCK1) (TREK-1 K+
DE CHANNEL SUBUNIT).
GN KCNK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

[1] SEQUENCE FROM N.A., FUNCTION AND TISSUE SPECIFICITY.
RP TISSUE-BRAIN: MEDLINE=97157476; PubMed=9003761.
RX Fluk M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RT "Cloning, functional expression and brain localization of a novel
RL unconventional outward rectifier K⁺ channel.";
RN EMBO J. 15:6854-6862(1996).
RP REVISIONS.
RC TISSUE-BRAIN:
RA Fluk M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RL Lazdunski M.;
RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fluk M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K⁺
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, U73488; AAC53005.2; -.
DR MGD; MG1:109366; Kcnnk2.
DR InterPro: IPR000099; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR003280; -.
DR Pfam: PF02034; TWIK channel; 1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DDDD103EFA05 CRC64;

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Cc      60  1 MKNOVFLLATLVCFTFLVGAANFADLESPELEIR...RODELBARVNLSGGGE
Cc      97  42 MKNKVTSTFLVLV--VLTLTIGAAVFAKEOPDOLSORP...LOKOTPLAQACVNS--T
Cc     108  61 ELERVLVL-LRPHKGKV-----QMRAGSEFYVA...TTIGYGHAPSTDGKV
Cc     157  98 ELDELDIQIVAAINNGIITPLGNSSNQVSHMDLGSSFFV...TITGCGNISPRREGGI
Cc     156  109 FCMETALLGIPLTVLMFOSLGERINTLVRYLYLRKKGI...KAD-----VSM
Cc     208  158 FCILIALLAGIPLFGFLTAGVGVDQLGTIF-----CK...KVEDTFIKMNVSOTKIRI
Cc     216  157 ANMWLIGFESCSTLCIAAASFHVEHHPTFOAYYYCF...LIGFGGVVALOKKOALOT
Cc     266  209 ISTTILIFGCULFPAALPAVLPIFKHEGMSALDAIFYVIL...LTGFGDVAGGSQ--LEY
Cc     274  217 QPOYAFSEFVVILTDTLVIGAFNLV--VLREPMTNAEI...ADAEHRALLFRNGAGGG
Cc     307  267 LDFYFPVWFWMLVLVALFAAVLNSIGIMLKRTISKTK...V-----
Cc     334  275 GGGSAHTTDTGASTTAAGGGRNYAELVHQSQCILVYSKRKLQYSLIPMLRPDL
Cc     340  -308 GEFRHAHAEMTA-----NVTAE-----FKETRRLSLVEI----YDKF
Cc     362  335 TSDTCVEOSHSPGGGGKRYSD-TPSRRL 362
Cc     369  341 QRATSVKRRKLSELAGLNHNDELTPCRRLL 369

RESULT      5
C1HW2_HUMAN STANDARD: PRT; 426 AA; TTIGYGHAPSTDGKV
DC 095069; 09UNE3;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TPKC1) (TREK-1 K+ CHANNEL SUBUNIT).
DE CNMK2 OR TREK.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99254548; PubMed=10321245;
RX Patel A.J., Honore E., Lesage F., Fink M., Boy G., Jazdzunski M., "Inhalational anesthetics activate two-pore domain background K+ channels.", Nat. Neurosci. 2:422-426(1999).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE-Brain;
DC Price L.A., Hellings S.E., Hayashi J.H., Patch M.H.; Submitted (Mar-1997) to the EMBL/GenBank/DBJ databases.
RL -1 FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1 SUBUNIT: HOMODIMER (POTENTIAL).
CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1 MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFURANE.
Cc -1 STABILITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
Cc -----
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Cc -----
Cc EMBL; AF129399; AAA047569.1; -

```


DB 235 VFWFLLGLAYFASVLTIGNMLRVSSRR-----TRAENGILTAQA 275
 QY 277 GSAHTTDTFASSTAAG 292
 DB 276 ASWGTGTATVATORAG 291

RESULT 7
 ID C1W4_MOUSE STANDARD; PRT: 398 AA.
 AC 088454; 01-OCT-2000 (Rel. 40, Created).
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-STIMULATED POTASSIUM CHANNEL PROTEIN) (TTRAK).
 GN KCNK4 OR TTRAK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98292450; PubMed=9628867;
 RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M., Lazdunski M.;
 RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids.";
 RL EMBO J. 17:3297-3308(1998).
 RN [2]
 RP ACTIVATION.
 RX MEDLINE=99254548; PubMed=10321245;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";
 RL Nat. Neurosci. 2:422-426(1999).
 CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH EXTERNAL K+ CONCENTRATIONS.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/TRAAT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND TESTIS.
 CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
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 CC -----
 CC EMBL: AF056492; AAC40181.1; -
 DR MGD: MGI:1298234; KCNK4.
 DR InterPro: IPR000099; -
 DR InterPro: IPR001622; -
 DR InterPro: IPR003280; -
 DR Pfam: PF02034; TWIK channel. 1.
 DR PRINTS: PR01333; 2PORECHANEL.
 KM Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein; Alternative splicing.
 KW DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 4 24 POTENTIAL.
 FT DOMAIN 1 13 PORE-FORMING (POTENTIAL).
 FT DOMAIN 89 113 PORE-FORMING (POTENTIAL).

FT TRANSMEM 119 139 POTENTIAL.
 FT DOMAIN 140 171 CYTOPLASMIC (PC, EHTIAL).
 FT TRANSMEM 172 192 POTENTIAL.
 FT DOMAIN 198 222 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 235 255 POTENTIAL.
 FT DOMAIN 256 398 POTENTIAL.
 FT CARBOHYD 81 81 N-LINKED (GLCN...) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCN...) (POTENTIAL).
 FT VARSPPLIC 63 67 KLIVE -> KAMAI (ISOFORM 2).
 FT VARSPPLIC 68 398 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7A834 CRC64;

Query Match 16.0%; Score 326.5; Ls: Length 398;
 Best Local Similarity 31.5%; Pred. No. 6; Ls: 1;
 Matches 85; Conservative 45; Mismatches 5; Indels 45; Gaps 7;

QY 9 LALIVCTFTYLLVGAFAVPALESEPELIERORLET-ROK VARRNLSGGVEELERVL 67
 DB 7 LALLALVLLVLYSGALVQALPHEQQAQKKMDHGRDQ LDPHCVSOKSLEDFFKLLV 66
 QY 68 RLKPKAGVQ-----WRPAGSFYFAIVTITTTT VAAASTDGGKVFCCFFYAL 115
 DB 67 EALGGGANPETSMTNSSNHSAMNLSAFAFFSGTITTTT VLVLTDPAGRLFCIFVAL 126
 QY 116 LGIPLTVLWFQSLGERINTLVRLYLHRAKKGGMRA-----DVSMMNVLI 162
 DB 127 VGIPFLGMLLAGVGRDGLSGSLR-----RGIGHIHAIFI VAVPGLVRLSLAVFLILI 179
 QY 163 GFECISITLCIGAAAFSHYEHMTFFQAYVYCCITLTIGFVSYVALOKDQALQTOPQY-- 220
 DB 180 G---CLLFVLFTFPFVSWSKLEAIFYVITLTGCF TRV--PGDGTGQNSPAYOP 234
 QY 221 -----VAESFVILIGLTYIGAFINLVYLR 245
 DB 235 LVWFVILGLAYFASVLTIGNMLRVSSRR 264

RESULT 8
 ID C1W1_HUMAN STANDARD; PRT: 336 AA.
 AC 000180; Q13307;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARDLY RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1) (POTASSIUM CHANNEL K.3.1.1).
 GN KCNK1 OR TWIK1 OR HOH01 OR KCNOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
 RC TISSUE=Kidney;
 RX MEDLINE=96183184; PubMed=8605869;
 RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G., Baranin J.;
 RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a novel structure.";
 RL EMBO J. 15:1004-1011(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND REVIEW.
 RC TISSUE=Brain;
 RX MEDLINE=98122696; PubMed=9462864;
 RA Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;
 RT "Sequence and function of the two P domain potassium channels: implications of an emerging superfamily.";
 RL J. Mol. Med. 76:13-20(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Desir G.V., Orlas M., Freeman T.;
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.

```

CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
CC -1- BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
CC -1- INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U36332; AAB01688.1; -.
CC DR EMBL: U76996; AAB97878.1; -.
CC DR EMBL: U90065; AAB51147.1; -.
CC DR MIM: 601745; -.
CC DR InterPro: IPR000099; -.
CC DR InterPro: IPR001622; -.
CC DR InterPro: IPR001779; -.
CC DR InterPro: IPR003280; -.
CC DR Pfam: PF02034; TWIK_channel; 1.
CC DR PRINTS: PRO1096; TWIKCHANNEL.
CC DR PRINTS: PRO1333; 2PORECHANNEL.
CC KM Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC Glycoprotein.
CC FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 21 41 POTENTIAL.
CC FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
CC FT TRANSSEM 133 153 POTENTIAL.
CC FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 178 198 POTENTIAL.
CC FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
CC FT TRANSSEM 247 267 POTENTIAL.
CC FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT MUTAGEN 161 161 T->A: NO EFFECT ON CHANNEL ACTIVITY.
CC SQ SEQUENCE 336 AA; 38143 MW; 2A41D950132315D CRC64;

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Query Match 15.7% Score 320.5; DB 1; Length 336;
Best Local Similarity 32.4%; Pred. No. 1.5e-18;
Matches 90; Conservative 47; Mismatches 102; Indels 39; Gaps 9;

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RESULT 9
CINS_HUMAN STANDARD; PRT; 499 AA.
ID CINS_HUMAN

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AC 095279;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL, SUBFAMILY K MEMBER 5 (ACT1, SENSITIVE POTASSIUM
DE CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL 2).
GN KCNK5 OR TASK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99030343; Pubmed=9812978;
RA Reyes R., Duprat F., Lesage F., Fink M., Sanguin M., Farman N.,
RA Lazdunski M.;
RT Cloning and expression of a novel pH-sensi two pore domain K+
RT channel from human kidney.
RL J. Biol. Chem. 273:30863-30869(1998).
CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION LOST AT HIGH EXTERNAL
CC K+ CONCENTRATIONS.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED
CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL
CC ACIDIFICATION.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF084830; AAC79458.1; -.
CC DR MIM: 603493; -.
CC DR InterPro: IPR000099; -.
CC DR InterPro: IPR001622; -.
CC DR InterPro: IPR003280; -.
CC DR Pfam: PF02034; TWIK_channel; 1.
CC DR PRINTS: PRO1333; 2PORECHANNEL.
CC KM Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC Glycoprotein.
CC FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 8 26 POTENTIAL.
CC FT DOMAIN 85 112 PORE-FORMING (POTENTIAL).
CC FT TRANSSEM 113 133 POTENTIAL.
CC FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 158 180 POTENTIAL.
CC FT DOMAIN 190 215 PORE-FORMING (POTENTIAL).
CC FT TRANSSEM 230 250 POTENTIAL.
CC FT CARBOHYD 251 325 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 77 77 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 499 AA; 55130 MW; E871A7A48231 CRC64;

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Query Match 15.6% Score 319; DB 1; Length 499;
Best Local Similarity 32.8%; Pred. No. 3.1e-18;
Matches 84; Conservative 47; Mismatches 102; Indels 28; Gaps 8;

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OY 18 YLVGAAVFDALSEPELIERORL ELROELRARNYLSOGYEELERVVRL 66
DB 15 YLVGAAVFDALSEPELIERORL ELROELRARNYLSOGYEELERVVRL 66
OY 67 -LRLPKHAGVQWRFGASFYFAITVITTYGYGAAP...KYFCMFALLGIPILVM 124

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RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-53.
 RC TISSUE-Brain;
 RA MEDLINE-99175162; PubMed-10075682;
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
 RT "TWIK-2, a new weak inward rectifying member of the tandem pore domain
 potassium channel family."
 RL J. Biol. Chem. 274:7887-7892(1999).
 RN [3]
 RP ERRATUM.
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
 RA Menta Y., Forsythe J.R., Yost C.S.;
 RL J. Biol. Chem. 274:24440-24440(1999).
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
 TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
 PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED
 IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
 CC -1- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL
 DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARBITUM.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CHANNELS.
 CC -----
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 CC -----
 DR EMBL: AF134149; AAD22980.1;
 DR EMBL: AF117708; AAD24000.1;
 DR MIM: 603939;
 DR InterPro: IPR001622;
 DR InterPro: IPR001779;
 DR PRINTS: PR01096; TWIK1CHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 5 25 POTENTIAL.
 FT DOMAIN 90 115 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 121 141 POTENTIAL.
 FT DOMAIN 142 172 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 173 193 POTENTIAL.
 FT DOMAIN 199 223 PORE-FORMING (POTENTIAL).
 FT TRANSSEM 236 256 POTENTIAL.
 FT DOMAIN 257 313 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOTAGN 53 53 C->A: NO CHANNEL ACTIVITY.
 FT SEQUENCE 313 AA; 33747 MW; 1379382DFB0575DE CRC64;
 SQ
 Query Match 14.58; Score 295.5; DB 1; Length 313;
 Best Local Similarity 31.78; Pred. No. 1,4e-16;
 Matches 90; Conservative 40; Mismatches 95; Indels 59; Gaps 12;
 Oy 18 YLVGAVFADLESEPELIERORLEKROELRARN-----LSGGYELE 63
 Db 17 YLVGALLVLRLESPHARLRAELLETIRALQLOKSPCAAPALDAFVERVLAAG---RLG 73
 Oy 64 RVLRLKPKHAGVQ---WRAGSFYATVTTTGYGHAPESTDGKVCFFVALLGLPT 120
 Db 74 RVLVLANSGSNASDPAMDPAFSAFLFASTLTITVGYGTPPLTDAGKAFAIAPALLGVP 133
 Oy 121 TLVNFQSLGKINLVRLVRLHRAKKGGM-----RADVSMANWVLGFSCSTLTC-- 172
 Db 134 TMLLTASQRLSL---LTHVPLSMLSMRWGMDPRRA---ACMHVALGVLVTVCF 186

Oy 173 IGAASFHYEH-WTFPOAYVYCFITLTIGFDYVALQFQA-ATQPO---YVAFSEVYI 228
 Db 187 VPAVIFAHLEAFMSFLDAFYCFISLTIGFDYVPGF---AFQCPYRALYKVLVTVYL 242
 Oy 229 LTGLT-----VIGAFNLVLRFPMT-----MR-DFKR 256
 Db 243 FLGLVAMVLYQTRHVSDDLGLTELILPPCPASFNL-LLR 286
 RESULT 12
 ORK1_DROME STANDARD; PRT; 1001 AA;
 AC 094526;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1, TWO PORE DOMAIN POTASSIUM
 CHANNEL ORK1.
 GN ORK1 OR CG1615.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Larva;
 RX MEDLINE-97075152; PubMed-8917578;
 RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Emsch M.H.;
 RT "ORK1, a potassium-selective leak channel with two pore domains
 cloned from Drosophila melanogaster by expression in Saccharomyces
 cerevisiae."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans J., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hosick R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhao Z., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Cline M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nee C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews S., Binkovoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraki A., Binkovoch C., Binkovoch E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
 RA Burkova D., Botchan M.R., Bouck J., Brooks D., Brothier P.,
 RA Burdick K.C., Busam D.A., Butler H., Cadieu C., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport J., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.E., Miller W.L., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rochet J., Dunkov B.G., Dunn P.,
 RA Foster C., Evangelista C.C., Ferraz C., Fierman J., Fierman S., Fleischmann W.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guo X., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei J.H., Iobagwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kelson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mobergerson D.,
 RA Merkulov G., Milshina N.V., Moberg C., Morris S., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murray D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard R., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Schmeidler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skir K.M.P., Smith T.,
 RA Spier E.C., Spradling A.C., Stapleton M., St. A., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu L., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

CHANNELS.

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CC EMBL: AF110521; AAD29577.1; ALT_TERM.

DR EMBL: AB015729; BA35074.1; -

DR EMBL: AF028220; AAD09337.1; -

DR EMBL: AF012324; AAF21603.1; -

DR EMBL: AF158234; AAF14528.1; -

DR MGI: 1341841; Kcnk8.

DR InterPro: IPR001622; -

DR InterPro: IPR003280; -

DR PRINTS: PRO1333; 2PORKCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Potassium transport;

KW Glycoprotein.

FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 11 31 POTENTIAL.

FT DOMAIN 92 118 PORE-FORMING (POTENTIAL).

FT TRANSMEM 120 140 POTENTIAL.

FT DOMAIN 141 172 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 173 193 POTENTIAL.

FT DOMAIN 199 227 PORE-FORMING (POTENTIAL).

FT TRANSMEM 233 253 POTENTIAL.

FT DOMAIN 254 307 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 1 3 MGS -> TR (IN REF. 4).

FT CONFLICT 2 3 GS -> TR (IN REF. 4).

FT CONFLICT 2 3 GS -> TR (IN REF. 4).

FT CONFLICT 84 84 G -> S (IN REF. 2, 3, 4 AND 5).

FT CONFLICT 231 232 YH -> SP (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

FT CONFLICT 293 293 T -> P (IN REF. 2).

Query Match 10.8%; Score 221; DB 1; Length 307;

Best Local Similarity 26.7%; Pred. No. 1.2e-10; Mismatches 119; Indels 46; Gaps 10;

Matches 76; Conservative 44; Mismatches 119; Indels 46; Gaps 10;

QY 7 RTIALIVCTFTYLVGAAPDALESEP--ELIERORLELRQOEIRARVNLSCGGYEELER 64

Db 9 RYLLLAHLAHLAMGLGAVVLALEGPARRHLQAVQALASFOAEHRACLPREALEELLG 68

QY 65 VVLRKPKKAGV-----QMRFAGSYFAITVTTTGYGHADPSTDGKVFQCFYA 114

Db 69 AVLRKQAH--GVSLGNGSETSNWDLPSALLFTASILTITTYGHMADPLSSGKAFQVYA 126

QY 115 ILGIPILVMEOSL-----GRINTIVRYLHRAKKGLGMRADVSMANMVLIG 163

Db 127 ALGIPASLAAVAALRHCLLPVFSRPGDV--AIRWOLAPAOAL-----LQAGLGL- 177

QY 164 FFSCTISLIGAAAFSHEHMTFFQAVYCYFTLTITGFDYVALQ--KQDALOTOPQY 220

Db 178 -VACVFLRLALVLMGQGCSSLALYFPGSGSLTGIDDLPAHGRGLHAPATYHLOF 236

QY 221 VAFSEVY--ILTGLTVIGAFNLVLRFTM-----NADEKRD 257

Db 237 ALIGYLLGLLAMLAVETFSFELPOVRAMVKFQPSGSRTEDED 281

Search completed: August 28, 2001, 17:13:15
 Job time: 409 sec

QY	241	LVLLEFMTNMNDEKRDDEHALLTLRRNGOAGGGG-----GGSAHTTDLTASSTAA-	291
Db	222	LVLLEFMTNMNDEKRDDEHALLTLHHNGOAGGLGSLCSGLSDGDVPRPDYVCAAG	261
QY	292	-----GGGGFRNVAEVLHFOSMCSCLMWKSKREKLOYSTIPMTIPRDLSTSPCEVS	343
Db	282	GMGVGVGGGGFRNVAEEMLHFOSMCSCLMWKSKREKLOYSTIPMTIPRDLSTSPCEVS	341
QY	344	HSSPRGGGGRYDTPSRRLCSGAPARSATISVSTGLHSLSTPRGLMKRRSSV	394
Db	342	HSSPRGGGGRYDTPSRHPLCSGTPRSATISVSTGLHSLATPRGLMKRRSSV	392

	RESULT	2	
909X34	ID	PRELIMINARY;	PRT; 299 AA.
AC	Q90X34;		
DT	01-MAY-2000 (TREMBLEL 13, Created)		
DT	01-MAY-2000 (TREMBLEL 13, Last sequence update)		
DT	01-MAR-2001 (TREMBLEL 16, Last annotation update)		
DE	PMUTATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
OX	NCBII_Taxid:10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,		
RL	Kaczmarek L.K.;		
RA	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF022821; AACD09338.1; -		
DR	InterPro; IPR000099; -		
DR	InterPro; IPR001622; -		
DR	InterPro; IPR003092; -		
DR	InterPro; IPR003280; -		
DR	Pfam; PF02034; TWIK-channel; 1.		
DR	PRINTS; PRO1333; ZPORECHANNEL.		
DR	PRINTS; PRO1095; TASKCHANNEL.		
KW	Ionic channel.		
FT	NON_TER 1 299 1		
SO	SEQUENCE 299 AA; 33325 MW; DCD41DBA212939C4 CRC64;		

Query Match	65.3%	Score 1333	DB 11	Length 299
Best Local Similarity	88.9%	Pred. No. 7.8e-110		
Matches 263	Conservative 7	Mismatches 18	Indels 8	Gaps 1

OY	4	ONVRLALIVCTFFYLLVGAIVFALISEPPIELROLELRODELRYARNLSOGGVEELE	63
Db	2	ENVRLALIVCTFFYLLVGAIVFALISEPPIELROLELROELRYARNLSSEGVEELE	61
OY	64	RVVLRLPKHAKGVOMRPAAGSFYFALITVITTYIGYHAAPSTDGCVFCMFYALLGIPLLV	123
Db	62	RVVLRLPKHAKGVOMRPAAGSFYFALITVITTYIGYHAAPSTDGCVFCMFYALLGIPLLV	121
OY	124	MEOSLGEPIINTLVRYLLHBRKAGKGMRRADYSMANMVLITPFSCISTLCIGAAAFSHYH	183
Db	122	MEOSLGERINTLVRYLLHBRKAGKGMRRADYSMANMVLITPFSCISTLCIGAAAFSTYER	181
OY	184	WTFPQAYVYCEFTLLTYIGFGDYVALQKDAQOTOPQYVAESFYVILTGLTVIGAFNLVY	243
Db	182	WTFPQAYVYCEFTLLTYIGFGDYVALQKDAQOTOPQYVAESFYVILTGLTVIGAFNLVY	241
OY	244	LRFPMMAEDKRPRAEHRALLTRNGKAGGGG-----GSAHNTDTTASSTAA	291
Db	242	LRFPMMAEDKRPRAEHRALLTRNGKAGGGG-----GSAHNTDTTASSTAA	297

RESULT 3
Q9ESM4
ID Q9ESM4 PRELIMINARY;
PRT; 301 AA.

AC Q9ESM4; 01-MAR-2001 (Tremblrel, 16, Created)
DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)
DE TWIK-RELATED ACID-SENSITIVE K+ CHANNEL SPLICED VARIANT (TASK1C).
GN KCNK3C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AOTRA;
RA Ohta S., Kitsuikawa M., Imaizumi Y.;
RT "TWIK-related acid-sensitive K+ channel (TA-K1) (KCNK3) splice
RT variant".
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB048824; BAB16711.1; -.
KW Ionic channel.
SQ SEQUENCE 301 AA; 32811 MW; 265DE3BDFA95959E CRC64;

Query Match	63.6%	Score 1298.5	118.11	Length 301
Best Local Similarity	85.0%	Pred. No. 8.8e-17		
Matches 256, Conservative	6	Mismatches 22	Indels 17	Gaps 2

QY	111	MEYALLIGPLTVNEOSIGERINTLVYLLHRAKKGKRAVSMANVLIGFSCIST	170
Db	1	MEYALLIGPLTVNEFOSIGERINTFVYRLHRAKRGJGMRH:EVSMANVVLIGVSCIST	60
QY	171	LCIGAAAFSHYEHTFEOAYYCCITLTLTIGFGDYALCKE:ALQTOPOVVAESFYVILT	230
Db	61	LCIGAAAFSYEERTFFQAYYCCITLTLTIGFGDYALCKD:JALQTOPOVVAESFYVILT	120
QY	231	GLTVIGAFNLVLREMTMAEDEKRDABHRALLTRNGCAAG:JOG-----GSAHTT	282
Db	121	GLTVIGAFNLVLRFMTMAEDEKRDABHRALLTHNGC:AL:JGGLSCISGSLGDDGVRPR	180
QY	283	DTASTTAA-----GGGGFNNVYAEVLHFOQSMOCSCLMT:SKREKLOYISPMILPRDL	333
Db	181	DPVTCAAAGMGVGVGGGFFNNVYAEMLHFOSMOCSCLMT:KSREKLOYISPMILPRDL	240
QY	334	STSDTCVEGSHSSPFGGGGRYSDTPSRRCLOCSGAPRSMISV:GLMSLSTFRGLMKRRSS	393
Db	241	STSDTCVEGSHSSPFGGGGRYSDTPSRHPCLOCSGQORSAISS:IGLHSLATFRGLMKRRSS	300
QY	394	V 394	
Db	301	V 301	

RESULT	4
09NPC2	
ID	09NPC2
AC	09NPC2;
DT	01-OCT-2000 (Tremblrel, 15, Created)
DT	01-OCT-2000 (Tremblrel, 15, last sequence update)
DT	01-MAR-2001 (Tremblrel, 15, last annotation update)
DE	2P DOMAIN POTASSIUM CHANNEL TASK-3 (POTASSIUM CHANNEL TASK3) (TWO PORE POTASSIUM CHANNEL KT3.2) (2P DOMAIN POTASSIUM CHANNEL).
GN	KCNK9.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Girard C., Lesage F., Lazdunski M.,
RT	"Human Task-3, a novel 2P domain potassium channel related to Task.",
RL	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=20287530; PubMed=10747866;

RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
 RA Karschin A., Derst C.;
 RT "TASK-3, a novel tandem pore domain acid-sensitive K⁺ channel. An
 RT extracellular histidine as pH sensor.";
 RL J. Biol. Chem. 275:16650-16657(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D.,
 RA Coetzee W., Rudy B.;
 RT "K7.2 and K7.3 Two Novel Human Two Pore K⁺ Channels Closely Related
 RT to TASK1.";
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX Pubmed=11042359;
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
 RA Kelsell R.E., Mordock P.R., Randall A.D., Rennie G.T., Gloger I.S.;
 RT "Cloning, localisation and functional expression of a novel human,
 RT cerebellum specific, two pore domain potassium channel.";
 RL Brain Res. Mol. Brain Res. 82:74-83(2000).
 DR EMBL: AF279809; AAF85982.1; -;
 DR EMBL: AF257080; AAG33126.1; -;
 DR EMBL: AF248241; AAG31730.1; -;
 DR InterPro: IPR000099; -;
 DR InterPro: IPR001622; -;
 DR InterPro: IPR003092; -;
 DR InterPro: IPR003280; -;
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PRO1333; ZPORECHANNEL.
 DR PRINTS: PRO1095; TASKCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 374 AA; 42263 MW; 8A19AE55AD7F38 CRC64;

Query Match 54.7%; Score 1116; DB 4; Length 374;
 Best Local Similarity 59.0%; Pred. No. 1.5e-90;
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELARVYNLSGGYE 60
 DB 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELARVYNLSGGYE 60
 QY 61 ELERVRLRKPKAGVOMRFAGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 DB 61 ELERVRLRKPKAGVOMRFAGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 QY 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 DB 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 QY 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 DB 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 QY 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 DB 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 QY 181 YEHTFPOAYYCFITLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 DB 181 YEHTFPOAYYCFITLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 QY 181 CEEVSFHAHYCYFTLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 DB 181 CEEVSFHAHYCYFTLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 300
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 300
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 300
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 300
 QY 301 -AEVLHROSQSCSLMYKSRKLOYSIPMIIPRLDSTDCVEGSHSBBGGGGRYSDP 359
 DB 301 -AEVLHROSQSCSLMYKSRKLOYSIPMIIPRLDSTDCVEGSHSBBGGGGRYSDP 359
 QY 287 KADVPDLOSQSCCYRSOD---YGGRSVAPQNSFAKLAPHYRHSISYKTEISPTLK 343
 DB 287 KADVPDLOSQSCCYRSOD---YGGRSVAPQNSFAKLAPHYRHSISYKTEISPTLK 343
 QY 360 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394
 DB 360 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394
 QY 344 NSLFP-----SPITSSIPGLSHSTHQRMLKRRKSV 374
 DB 344 NSLFP-----SPITSSIPGLSHSTHQRMLKRRKSV 374

RESULT 5
 ID 09JUL58 PRELIMINARY; PRT; 365 AA.
 AC 09JUL58;
 OC 09JUL58;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation)
 DE POTASSIUM CHANNEL TASK3.
 OS KNKCN.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathae; Muridae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=20287530; Pubmed=10747866;
 RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
 RA Karschin A., Derst C.;
 RT "TASK-3, a novel tandem pore domain acid-sensitive K⁺ channel. An
 RT extracellular histidine as pH sensor.";
 RL J. Biol. Chem. 275:16650-16657(2000).
 DR EMBL: AF212827; AAF63706.1; -;
 DR InterPro: IPR000099; -;
 DR InterPro: IPR001622; -;
 DR InterPro: IPR003092; -;
 DR InterPro: IPR003280; -;
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PRO1333; ZPORECHANNEL.
 DR PRINTS: PRO1095; TASKCHANNEL.
 SQ SEQUENCE 365 AA; 40769 MW; 261DC973FF5 CRC64;

Query Match 52.4%; Score 1069.5; DB 4; Length 365;
 Best Local Similarity 57.1%; Pred. No. 1.9e-90;
 Matches 226; Conservative 43; Mismatches 96; Indels 33; Gaps 6;

QY 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELARVYNLSGGYE 60
 DB 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELARVYNLSGGYE 60
 QY 61 ELERVRLRKPKAGVOMRFAGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 DB 61 ELERVRLRKPKAGVOMRFAGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 QY 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 DB 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYGAAPSTDGKVFYCMFVALLGIP 120
 QY 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 DB 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 QY 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 DB 121 TLVFOSLGERINFLVRLHRAKGLGMRADVSMANVLIGFSCISTLCIGAAAFSH 180
 QY 181 YEHTFPOAYYCFITLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 DB 181 YEHTFPOAYYCFITLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 QY 181 CEEVSFHAHYCYFTLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 DB 181 CEEVSFHAHYCYFTLTIGFGDYVALQKQALOTQPOYVAFSEVYITLGLTVIGAF 240
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 298
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 298
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 298
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTPASSTAAGGGGFRNV 298
 QY 299 VYAEVLHROSQSCSLMYKSRKLOYSIPMIIPRLDSTDCVEGSHSBBGGGGRYSDP 358
 DB 299 VYAEVLHROSQSCSLMYKSRKLOYSIPMIIPRLDSTDCVEGSHSBBGGGGRYSDP 358
 QY 292 -----DLOSVCSCACYRSDP--ONFGATLAPDPLHS SRIEFT-----SPS 331
 DB 292 -----DLOSVCSCACYRSDP--ONFGATLAPDPLHS SRIEFT-----SPS 331
 QY 359 RRCCLSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394
 DB 359 RRCCLSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394
 QY 332 --TLKNSLFPSPISSVSPGLHSFGDNHRLMKRRSV 365
 DB 332 --TLKNSLFPSPISSVSPGLHSFGDNHRLMKRRSV 365

RESULT 6
 ID 09JUL58 PRELIMINARY; PRT; 395 AA.
 AC 09JUL58;
 OC 09JUL58;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation)
 DE POTASSIUM CHANNEL TASK3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathae; Muridae; Rattus.

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE D0781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE POTASSIUM
 CHANNEL PROTEIN TASK (KCNK3)).
 GN D0781B1.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lovell J.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL118522; CAC14068.1;
 SQ SEQUENCE 330 AA; 36222 MW; 24F428721A1C7790 CRC64;

Query Match 41.08; Score 838; DB 4; Length 330;
 Best Local Similarity 64.38; Pred. No. 4.8e-66;
 Matches 166; Conservative 32; Mismatches 60; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLEKROELRARNLSGGYE 60
 1
 Db 1 MRRSVRAAGVILCTCTCLLVGAAVFDALSEALSGRORLVOKRGALRRKFGSAEDYR 60
 1
 QY 61 ELEERVLRKPKAGVOMRFGSFYFAITVTTTIGYHAAPSTDGKVCFCMFAALLGIP 120
 1
 Db 61 ELERLALQAEHRAGROKPFSGFYFAITVTTTIGYHAAPSTDGKVCFCMFAALLGIP 120
 1
 QY 121 TLVNFOSIGERINTLVRLHRAKKGMRADVSMMANVLIGFSCSTICGAAAFSH 180
 1
 Db 121 TLVNFOSIGERINTLVRLHRAKKGMRADVSMMANVLIGFSCSTICGAAAFSH 180
 1
 QY 181 YEHMTFFQAYYCFITTTTIGFGDYVALOKDOALOTOPYAFSEVYLTGTYIGAF 240
 1
 Db 181 FEGTTFHAYYYCTTTTIGFGDYVALOKDOALOTOPYAFSEVYLTGTYIGAF 240
 1
 QY 241 LVLRFTMTNADEKRD 258
 1
 Db 241 LVLRFTMTNADEKRD 258
 1

RESULT 10
 ID 076795 PRELIMINARY; PRT; 329 AA.
 AC 076795;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DE POTASSIUM CHANNEL SUBUNIT N2P38.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang Z.-W., Salkoff L.;
 RT "Potassium channels in C. elegans."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF083652; AAC32863.1;
 DR InterPro: IPR000099;
 DR InterPro: IPR001622;
 DR InterPro: IPR003280;
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PR01333; 2PORKCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 329 AA; 36992 MW; 338A6D9A577464CD CRC64;

Query Match 40.28; Score 820; DB 5; Length 329;
 Best Local Similarity 48.38; Pred. No. 1.8e-64;
 Matches 172; Conservative 54; Mismatches 84; Indels 46; Gaps 7;
 QY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLEKROELRARNLSGGYE 60

Db 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLEKROELRARNLSGGYE 60
 1
 QY 61 ELEERVLRKPKAGVOMRFGSFYFAITVTTTIGYHAAPSTDGKVCFCMFAALLGIP 120
 1
 Db 61 ELEERVLRKPKAGVOMRFGSFYFAITVTTTIGYHAAPSTDGKVCFCMFAALLGIP 120
 1
 QY 121 TLVNFOSIGERINTLVRLHRAKKGMRADVSMMANVLIGFSCSTICGAAAFSH 180
 1
 Db 121 TLVNFOSIGERINTLVRLHRAKKGMRADVSMMANVLIGFSCSTICGAAAFSH 180
 1
 QY 179 SHYEMTFFQAYYCFITTTTIGFGDYVALOKDOALOTOPYAFSEVYLTGTYIGAF 238
 1
 Db 178 SSYEMTFFQAYYCFITTTTIGFGDYVALOKDOALOTOPYAFSEVYLTGTYIGAF 237
 1
 QY 239 LNLVLRFTMTNADEKRD 258
 1
 Db 238 LNLVLRFTMTNADEKRD 258
 1
 QY 295 GFRNVVAEVLHFGSMCSCLWYKRSREKLQYSIPMLIPRI 350
 1
 Db 293 GFRNVVAEVLHFGSMCSCLWYKRSREKLQYSIPMLIPRI 350
 1

RESULT 11
 ID 017185 PRELIMINARY; PRT; 336 AA.
 AC 017185;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DE F34D6.3 PROTEIN.
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE F34D6.3 PROTEIN.
 GN F34D6.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RA MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Ainscough R., Anderson K., Bayne C., Cooper J., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copestake R., Fawcett D., Fulton L.,
 RA Craxton M., Dear S., Du Z., Durbin R., Fawcett D., Fulton L.,
 RA Gardner A., Green P., Hawkins J., Laister N., Laister N., Laister N.,
 RA Jones M., Kershaw J., Kistner J., Laister N., Laister N., Laister N.,
 RA Lightning J., Lloyd C., McMurray A., Mortimer J., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Sainsbury D., Sainsbury D.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaudin M., Vaudin M., Vaudin M.,
 RA Watson A., Watsonstock L., Wilkinson-Spratt J., Wilkinson-Spratt J.,
 RT "2.2 Mb of contiguous nucleotide sequence of the chromosome III of C.
 elegans."
 RT Nature 368:32-38(1994).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RA Murray J., Wohlmann P., O'Neal D.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF025454; AAC71151.1;
 DR InterPro: IPR000099;
 DR InterPro: IPR001622;
 DR InterPro: IPR003280;
 DR Pfam: PF02034; TWIK_channel; 1.
 DR PRINTS: PR01333; 2PORKCHANNEL.
 SQ SEQUENCE 336 AA; 37700 MW; E0474024F69FC27E CRC64;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Manalidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flooker A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,
RA Palazolo D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
DR EMBL: AEO03701; AAF54970.1;
DR FlyBase: FBgn0038165; CG9637.
DR InterPro: IPR000099;
DR InterPro: IPR001622;
DR InterPro: IPR003092;
DR Pfam: PF02034; TWIK channel; 1.
DR PRINTS: PRO1095; TASKCHANNEL.
SQ SEQUENCE 398 AA; 44269 MW; D5DC01E9DBA6D7E CRC64;

Query Match 36.3%; Score 742; DB 5; Length 398;
Best Local Similarity 42.8%; Pred. No. 1.8e-57;
Matches 161; Conservative 65; Mismatches 76; Indels 74; Gaps 9;
QY 1 MKRONVRLIIVCTFTYLLVGAIVFDALSEPELIERORLEKQOELRARNISOGYE 60
DB 1 MKRONVRLIIVCTFTYLLVGAIVFDALSEPELIERORLEKQOELRARNISOGYE 60
QY 61 ELERVLRLKHKAGVDFGAFYFATVTTTIGYHAPSDGKFCFVALLG 120
DB 61 VMEIVVLKSEHKAGQKFGAFYATVTTTIGYHSTSTVGKLFMCIALVGLP 120
QY 121 TLVNFOSLGERINTLVRYLRLHARKGLGMRADYSMANVLIIGFSCISTLCI--GA 178
DB 121 GLVNFOSLGERINTLVRYLRLHARKGLGMRADYSMANVLIIGFSCISTLCI--GA 178
QY 179 SHYEMTFFOAYYYCFTLTITIGDYVALOKDOLQPOPYAVAFYITLGLVIGAF 238
DB 179 SKFGMSYFDSVYCYFTLTITIGDYVALQDNLNRPYVAFILFIFGLAIVAS 228
QY 239 LNLVLRPTNNADEKDAEHRAL-----LTERNGAGGGGGGSAHTTDT 285
DB 239 LNLVLRPTNNADEKDAEHRAL-----LTERNGAGGGGGGSAHTTDT 285
QY 286 SSTAAAGGGGRNVYAEVLAFQSMCSC-----LWYRSREK-- 320

DB 288 NTS-----SMCSCHICLGNRHH-----EKNDAENQYLRQSP 328
QY 321 -LOYSIPIIP-RDLS 334
DB 329 HIRLLEPVPMDLN 344
RESULT 14
ID 09JL57 PRELIMINARY; PRT: 270 A
AC 09JL57
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence)
DT 01-MAR-2001 (Tremblrel. 16, last annotatio
DE POTASSIUM CHANNEL TASK3 (FRAGMENT).
GN KCNK9.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Ve
OC Mammalia; Eutheria; Rodentia; Hystriognath
OX NCBI_TaxID=10141;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20287530; PubMed=10747866;
RA Rajan S., Witschmeyer E., Liu G.X., Preisig
RA Rajan S., Witschmeyer E., Liu G.X., Preisig
RT "TASK-3, a novel tandem proe domain acid-
RT extracellular histidine as pH sensor."
RT J. Biol. Chem. 275:16650-16657(2000).
DR EMBL: AF212828; AAF63707.1;
DR InterPro: IPR000099;
DR InterPro: IPR001622;
DR InterPro: IPR003092;
DR Pfam: PF02034; TWIK channel; 1.
DR PRINTS: PRO1095; TASKCHANNEL.
FT NON_TER 1 1
SQ SEQUENCE 270 AA; 29658 MW; 092ABPFC67E

Query Match 35.9%; Score 732.5; Length 270;
Best Local Similarity 54.2%; Pred. No. 7.8e-13;
Matches 163; Conservative 26; Mismatches 13; Indels 33; Gaps 6;
QY 96 YGHAPSTDGKVCMEFALLGIPTLVFOSLGERIN-----LHRAKGLGMRADYS 155
DB 1 YGHAPSTDGKVCMEFALLGIPTLVFOSLGERIN-----LHRAKGLGMRADYS 155
QY 156 MANVLIIGFSCISTLCIGAAAFSHYEHVTPFOAYY-----ITFGDYVALOKDOLQ 215
DB 61 MENNVTVGFFSCMGITLCIGAAAFSCCEMSFFHAYY-----ITFGDYVALOKDOLQ 120
QY 216 TOPQVAFSFYIITGLVIGAPLNLVLRPTNNAF-----EHRALLTNGAGGGGG 275
DB 121 RKPEYVAASFYIITGLVIGAPLNLVLRPTNNAF-----EHRALLTNGAGGGGG 275
QY 276 GGSATHTDTASTTAA--AGGGGRNVYAEVLAFQSMC-----KSNKELQYSIPMIIPDL 333
DB 175 SVVTHHISEAQQVQRNRYBEGG-----DIQSVG-----YRSDP--QNGCATLAPPL 223
QY 334 STSDTCVQSHSSPQGGGGGYSDDPSRRLCSGAPRSA-----VSGLHSLSTRGLMKRRSS 393
DB 224 HSLSCRIEEL-----SPS--TLKNSLFPSP-----SPSHSGFDNHRRLRRKS 269
QY 394 V 394
DB 270 V 270
RESULT 15
ID 076790 PRELIMINARY; PRT: 364 A
AC 076790;
DT 01-NOV-1998 (Tremblrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PUTATIVE POTASSIUM CHANNEL SUBUNIT N2P20.
GN TWK-4.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Z.-W., Salikoff L.;
RT "Potassium channels in *C. elegans*."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hendry C.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode *C. elegans*: A platform for
RT investigating biology";
RL Science 282:2012-2018(1998).
DR EMBL, AF083646; AAC32857.1; -.
DR EMBL, Z70266; CAB61045.1; -.
DR InterPro: IPR000099; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR003280; -.
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PR01333; 2PORECHANNEL.
KW Ionic channel.
SQ SEQUENCE 364 AA: 41374 MW: 424746050CCAC313 CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:06:26 ; Search time 21.03 Seconds

(without alignments)
669.472 Million cell updates/sec

Title: US-09-503-089a-2

Perfect score: 2100
Sequence: 1 MAAPDLDPKSAONSKPRL.....LNGLTPHCAGEIAYENIK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2062	98.2	426	CIW2_HUMAN	095069 homo sapien
2	2041	97.2	411	CIW2_MOUSE	P97438 mus musculu
3	803	38.2	393	CIW4_HUMAN	Q9ny98 homo sapien
4	776.5	37.0	398	CIW4_MOUSE	088454 mus musculu
5	427	20.3	499	CIW5_HUMAN	095279 homo sapien
6	379.5	18.1	336	CIW1_HUMAN	000180 homo sapien
7	370.5	17.6	336	CIW1_MOUSE	008581 mus musculu
8	363	17.3	394	CIW3_HUMAN	014649 homo sapien
9	348	16.6	313	CIW6_HUMAN	09y257 homo sapien
10	343	16.3	409	CIW3_MOUSE	035111 mus musculu
11	343	16.3	411	CIW3_RAT	054912 rattus norv
12	319	15.2	1001	ORX1_DROME	094526 drosophila
13	296.5	14.1	307	CIW8_MOUSE	092251 mus musculu
14	291.5	13.9	307	CIW7_HUMAN	Q9y242 homo sapien
15	217.5	10.4	335	TKW8_CAEEL	P34410 caenorhabdi
16	217.5	10.4	691	TKW1_YEAST	P40310 saccharomyc
17	121	5.8	228	YWS1_CAEEL	010937 caenorhabdi
18	120	5.7	676	CIW1_HUMAN	P51787 homo sapien
19	119	5.7	604	CIW1_MOUSE	P97414 mus musculu
20	106.5	5.1	334	PIT1_RHIME	030439 thizobium m
21	105.5	5.0	461	YIFK_SALTY	P37456 salmonella
22	104.5	5.0	649	QOX1_BACSU	P34956 bacillus su
23	102.5	4.9	362	SSR5_MOUSE	008858 mus musculu
24	102	4.9	402	Y718_METJA	058128 methanococ
25	102	4.9	451	Y5Y3_RHIME	033683 rhizobium m
26	101.5	4.8	342	COBD_SYNY3	P74475 synechocyst
27	100.5	4.8	352	Y436_METJA	Q57898 methanococ
28	100.5	4.8	476	MELB_SALTY	P30878 salmonella
29	100	4.8	333	OAC_BPSF6	P23214 bacterioph
30	100	4.8	395	CDSA_MYCPN	P75160 m putative
31	100	4.8	567	COX1_EMENT	P00402 emeticella
32	99.5	4.7	831	NAH3_RAT	P26433 rattus norv
33	99.5	4.7	834	NAH3_HUMAN	P48764 homo sapien

34	99.5	4.7	872	1	ATCL_MYCPN	P78036 mycoplasma
35	98.5	4.7	400	1	TYRP_HABIN	P44727 haemophilus
36	98.5	4.7	555	1	NRM1_CHICK	P51027 gallus gall
37	98.5	4.7	839	1	NAH3_DIDMA	028362 didelphis m
38	98	4.7	305	1	CDSA_MYCCE	049433 m putative
39	98	4.7	394	1	YDZC_SCHPO	010260 schizosacch
40	98	4.7	579	1	YH83_SCHPO	095522 schizosacch
41	97.5	4.6	412	1	085D_DROME	09vha2 drosophila
42	97.5	4.6	832	1	NAH3_RABIT	P26432 oryctolagus
43	97	4.6	333	1	Y13B_METJA	057604 methanococ
44	96.5	4.6	1036	1	SMO_DROME	P91682 drosophila
45	96	4.6	519	1	YF86_HABIN	P44263 haemophilus

ALIGNMENTS

RESULT	1	STANDARD	PRT	426 AA
CIW2_HUMAN				
ID	095069; Q9UNE3			
AC	01-OCT-2000 (Rel. 40, Created)			
DF	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTW) RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1 (TWO-PORE POTASSIUM CHANNEL SUBUNIT).			
GN	KCNK2 OR TREK.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99254548; PubMed-10321245;			
RA	Patel A.J., Honore E., Lesage F., Fink M., Hom G., Lazdunski M.;			
RT	"Inhalational anesthetics activate two-pore-domain background K ⁺ channels.";			
RL	Nat. Neurosci. 2:422-426(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TTSUB-Brain;			
RA	Price L.A., Hellings S.E., Hayashi J.H., Patil M.H.;			
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBI databases.			
CC	- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.			
CC	- SUBUNIT: HOMODIMER (POTENTIAL).			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE.			
CC	- MISCELLANEOUS: ACTIVATED BY VOLATILE GASES. ANAESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFLURANE.			
CC	- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.			
CC	This SWISS-PROT entry is copyright. It is provided through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as the content is in no way modified and this statement is not removed. The copyright is held by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	EMBL: AF129399; AAD47569.1; -			
DR	EMBL: AF004711; AAD01203.1; -			
DR	MM: 603219; -			
DR	InterPro: IPR000099; -			
DR	InterPro: IPR001622; -			
DR	InterPro: IPR003280; -			
DR	Pfam: PF02034; TWIK_Channel; 1.			
DR	PRINTS: PR01333; ZPORKCHANNEL.			
KW	Ionic channel; Transmembrane; Ion transport; Potassium transport;			
KW	Glycoprotein.			
FT	DOMAIN 1 61			CYTOSOLASMIC (POTENTIAL).
FT	TRANSMEM 62 82			POTENTIAL.
FT	DOMAIN 144 170			PORE-FORMING (EXTRACELLULARITY).

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FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 253 283 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 288 308 POTENTIAL.
FT DOMAIN 309 426 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY (BY SIMILARITY).
FT DOMAIN 354 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY
SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).
FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).
FT CONFLICT 391 391 S -> N (IN REF. 2).
FT CONFLICT 411 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 47016 MW; 2ABR2336D4009F4E CRC64;

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Query Match          98.2%; Score 2062; DB 1; Length 426;
Best local Similarity 98.5%; Pred. No. 1,le-130;
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 60
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DB 16 VAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 75
QY 61 GATVFKALDQPHETISORTTIVIOKOTFISQHSQVNSTEDELQOIVAAINAGIIPLGNT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 76 GATVFKALDQPHETISORTTIVIOKOTFISQHSQVNSTEDELQOIVAAINAGIIPLGNT 135
QY 121 SNOISIMDLSSFFPAGVTYTTIGFNGISPRTEGKIFCIYALGLIPGLFAGVGDQ 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 136 SNOISIMDLSSFFPAGVTYTTIGFNGISPRTEGKIFCIYALGLIPGLFAGVGDQ 195
QY 181 LGTIFGKGLAKVEDTEIKMNSQTKIRIISTILIFLGCVLFAVLAIPKHEIGMSALD 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 196 LGTIFGKGLAKVEDTEIKMNSQTKIRIISTILIFLGCVLFAVLAIPKHEIGMSALD 255
QY 241 AITFYVITTTTIGFDYVAGSGDIEYLDPKPYVMWILVGLAFPAVASMIGDMLRVIS 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 256 AITFYVITTTTIGFDYVAGSGDIEYLDPKPYVMWILVGLAFPAVASMIGDMLRVIS 315
QY 301 KKTKEVGEFRAHAEMTANVTAEFKETRRLSEVETDKFORATSIKRLSLAELAGNHQ 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 316 KKTKEVGEFRAHAEMTANVTAEFKETRRLSEVETDKFORATSIKRLSLAELAGNHQ 375
QY 361 ELTPCRRITLSVNHLENERDYLPLLTKESTIYNGLTTPHCAGEIAYENIK 411
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 376 ELTPCRRITLSVNHLENERDYLPLLTKESTIYNGLTTPHCAGEIAYENIK 426

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RESULT 2
CIN2_MOUSE STANDARD; PRT; 411 AA.
ID CIN2_MOUSE
AC P97438;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DE 01-OCT-2000 (Rel. 40; Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TPCK1) (TREK-1 K+
CHANNEL SUBUNIT).
DE GN KCN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RA MEDLINE=97157476; PubMed=9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;

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RT "Cloning, functional expression and brain localization of a novel
RT unconv. conditional outward rectifier K+ channel].
RL EMBO J. 15:6854-6862(1996).
RN [2]
RP REVISIONS.
RC TISSUE=Brain;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RP ACTIVATION
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore K+ channels in background K+
RT channels."
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN PREFRONTAL BULB.
CC HIPPOCAMPUS AND CEREBELLUM.
CC -1- MISCELLANEOUS: INHIBITED BY BARITUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
CC This SWISS-PROT entry is copyright. It is provided through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL: U73488; AAC53005.2; -.
CC DR MGD: MGI:109366; KCN2.
CC DR InterPro: IPR000099; -.
CC DR InterPro: IPR001622; -.
CC DR InterPro: IPR003280; -.
CC DR Pfam: PF02034; TWIK_channel.1.
CC DR PRINTS: PRO1333; 2PORECHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC Glycoprotein.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EFD05 CRC64;

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Query Match          97.2%; Score 2041; DB 1; Length 411;
Best local Similarity 96.1%; Pred. No. 2,7e-125;
Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GATVFKALDQPHETISORTTIVIOKOTFISQHSQVNSTEDELQOIVAAINAGIIPLGNT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
 CC EXTERNAL K+ CONCENTRATIONS.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND
 CC 2/TRANSP/TRANSCATD; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
 CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
 CC TESTIS.
 CC -1- MISCELLANEOUS: ACTIVATED BY ARCHIDONIC ACID AND OTHER UNSATURATED
 CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANESTHETICS SUCH AS
 CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC -----
 CC EMBL: AF056492; AAC40181.1; -.
 CC DR MGD: MGI:1298234; Kcnk4.
 CC DR InterPro: IPR000099; -.
 CC DR InterPro: IPR001622; -.
 CC DR InterPro: IPR003280; -.
 CC DR Pfam: PF02034; TWIK_Channel; 1.
 CC DR PRINTS: PR01333; 2PORECHANNEL.
 CC DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 CC Glycoprotein; Alternative splicing.
 CC FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 4 24 POTENTIAL.
 CC FT DOMAIN 89 113 PORE-FORMING (POTENTIAL).
 CC FT TRANSMEM 119 139 POTENTIAL.
 CC FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 172 192 POTENTIAL.
 CC FT DOMAIN 198 222 PORE-FORMING (POTENTIAL).
 CC FT TRANSMEM 235 255 POTENTIAL.
 CC FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 81 81 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 84 84 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT VARSPPLIC 63 67 KLVVE -> KAMAI (IN ISOFORM 2).
 CC FT VARSPPLIC 68 398 MISSING (IN ISOFORM 2).
 CC SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AEC92 CRC64;

Query Match 37.0%; Score 776.5; DB 1; Length 398;
 Best Local Similarity 49.8%; Pred. No. 5.1e-45;
 Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;

QY 42 MKKRTVSTFLVYVLIIGATVFKALEOPHEISORTTIVIOKOTFISQHSVCNSTELDE 101
 DB 1 MRSTTLALALALVLALEVFQALQEPHEQQAOKKMDHGRDPLRHPKSOXKSLD 60
 QY 102 LIOQVAAINAGTIP---LGNTSNOISHDIGSFEFFAGVTITTFGNSPTBEKGKIF 158
 DB 61 FIKLIVLEAGGANPETSMNTSSNHNLSAFAFFSGTITITIGNVLHTDGRLE 120
 QY 159 CIYVALGIPLEGFLAGVGDQGTGEGKIAKVEDTFIKMNVSQRIITSTIFELFG 218
 DB 121 CIFYVALVGPILGMLAGVDRGSLRGIGIEAIFLKNHPPGLVSLAVFLLLG 180
 QY 219 CULFVALPPIIRKHIEGMSALDAIVFVITLTTFGIDYVAGGSDIEYIDFKYVPMWFI 278
 DB 181 CLIFVLTLPFVFSYMSKLELAIVFVITLTTFVGDYVPPGDSQNSPAYOPLVPMFI 240
 QY 279 LVGLAFVAVLISMGDMLEVKSTKEEVEGFRAHAAEWNTANTYA 323
 DB 241 LGLAIFASVLTITIGNMLRAVSRTRAEKMGGLTAQAASWTGTVTA 285

RESULT 5
 CITE5_HUMAN STANDARD: PRT; 499 AA
 ID 095279;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACID-SENSITIVE POTASSIUM
 DE CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL 2).
 GN KCNKS OR TASK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE=99030343; PubMed=9812978;
 RA Reyes R., Duprat F., Lesage F., Fink M., Saubermann M., Farnan N.,
 RT Lazdunski M.,
 RT "Cloning and expression of a novel pH-sens. two pore domain K+
 RT channel from human kidney."
 RL J. Biol. Chem. 273:30863-30869(1998).
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL
 CC K+ CONCENTRATIONS.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
 CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL
 CC ACIDIFICATION.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC -----
 CC EMBL: AF084830; AAC79458.1; -.
 CC DR MIM: 603493; -.
 CC DR InterPro: IPR000099; -.
 CC DR InterPro: IPR001622; -.
 CC DR InterPro: IPR003280; -.
 CC DR Pfam: PF02034; TWIK_Channel; 1.
 CC DR PRINTS: PR01333; 2PORECHANNEL.
 CC DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 CC Glycoprotein.
 CC FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 8 26 POTENTIAL.
 CC FT DOMAIN 85 112 PORE-FORMING (POTENTIAL).
 CC FT TRANSMEM 113 133 POTENTIAL.
 CC FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 158 180 POTENTIAL.
 CC FT DOMAIN 190 215 PORE-FORMING (POTENTIAL).
 CC FT TRANSMEM 230 250 POTENTIAL.
 CC FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 77 77 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823D706 CRC64;

Query Match 20.3%; Score 427; DB 1; Length 499;
 Best Local Similarity 31.1%; Pred. No. 1.3e-21;
 Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;

QY 54 VVYLIIIGATVFKALEOPHEISORTTIVIOKOTFISQHSVCNSTELDELIOQVAAINAG 113

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Cc -----
Cc EMBL: U33632; AAB01688.1; -
Cc DR EMBL: U76966; AAB97878.1; -
Cc DR EMBL: U90065; AAB51147.1; -
Cc DR MIM: 601745; -
Cc DR InterPro: IPR000099; -
Cc DR InterPro: IPR001622; -
Cc DR InterPro: IPR001779; -
Cc DR InterPro: IPR003280; -
Cc DR Pfam: PF02034; TWIK_channel; 1.
Cc DR PRINTS: PR01096; TWIK1CHANNEL.
Cc DR PRINTS: PR01333; 2PORKCHANNEL.
Cc KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
Cc Glycoprotein.
Cc FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
Cc FT TRANSMEM 21 41 PORE-FORMING (POTENTIAL).
Cc FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
Cc FT TRANSMEM 133 153 POTENTIAL.
Cc FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
Cc FT TRANSMEM 178 198 POTENTIAL.
Cc FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
Cc FT TRANSMEM 247 267 CYTOPLASMIC (POTENTIAL).
Cc FT DOMAIN 268 336 N-LINKED (GLYCOPOLYMER) (POTENTIAL).
Cc FT CARBOHYD 95 95 T->A: NO EFFECT ON CHANNEL ACTIVITY.
Cc FT MUTAGEN 161 161
Cc SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;

RESULT 6
CIT1_HUMAN STANDARD; PRT; 336 AA.
AC 000180; Q13307;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TWIK-1) (POTASSIUM CHANNEL KCNO1).
GN KCNK1 OR TWIK1 OR HOHOL OR KCNO1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
RC TISSUE=Kidney;
RX MEDLINE=96183184; PubMed=8605869;
RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
RA Barhanin J.;
RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a
RT novel structure."
RL EMBL J. 15:1004-1011(1996).
RN [2]
RP SEQUENCE FROM N.A., AND REVIEW.
RC TISSUE=Brain;
RX MEDLINE=98122696; PubMed=9462864;
RA Goldstein S.A.N., Wang K.-W., Iian N., Pausch M.H.;
RT "Sequence and function of the two P domain potassium channels:
RT Implications of an emerging superfamily."
RL J. Mol. Med. 76:13-20(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Desir G.V., Orlas M., Freeman T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
CC BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
CC INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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Cc -----
Cc EMBL: U33632; AAB01688.1; -
Cc DR EMBL: U76966; AAB97878.1; -
Cc DR EMBL: U90065; AAB51147.1; -
Cc DR MIM: 601745; -
Cc DR InterPro: IPR000099; -
Cc DR InterPro: IPR001622; -
Cc DR InterPro: IPR001779; -
Cc DR InterPro: IPR003280; -
Cc DR Pfam: PF02034; TWIK_channel; 1.
Cc DR PRINTS: PR01096; TWIK1CHANNEL.
Cc DR PRINTS: PR01333; 2PORKCHANNEL.
Cc KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
Cc Glycoprotein.
Cc FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
Cc FT TRANSMEM 21 41 PORE-FORMING (POTENTIAL).
Cc FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
Cc FT TRANSMEM 133 153 POTENTIAL.
Cc FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
Cc FT TRANSMEM 178 198 POTENTIAL.
Cc FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
Cc FT TRANSMEM 247 267 CYTOPLASMIC (POTENTIAL).
Cc FT DOMAIN 268 336 N-LINKED (GLYCOPOLYMER) (POTENTIAL).
Cc FT CARBOHYD 95 95 T->A: NO EFFECT ON CHANNEL ACTIVITY.
Cc FT MUTAGEN 161 161
Cc SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;

Query Match 18.1%; Score 379.5; Length 336;
Best Local Similarity 32.5%; Pred. No. 1.2e-1;
Matches 90; Conservative 62; Mismatches 11; Indels 17; Gaps 9;

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Cc -----
Cc EMBL: U33632; AAB01688.1; -
Cc DR EMBL: U76966; AAB97878.1; -
Cc DR EMBL: U90065; AAB51147.1; -
Cc DR MIM: 601745; -
Cc DR InterPro: IPR000099; -
Cc DR InterPro: IPR001622; -
Cc DR InterPro: IPR001779; -
Cc DR InterPro: IPR003280; -
Cc DR Pfam: PF02034; TWIK_channel; 1.
Cc DR PRINTS: PR01096; TWIK1CHANNEL.
Cc DR PRINTS: PR01333; 2PORKCHANNEL.
Cc KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
Cc Glycoprotein.
Cc FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
Cc FT TRANSMEM 21 41 PORE-FORMING (POTENTIAL).
Cc FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
Cc FT TRANSMEM 133 153 POTENTIAL.
Cc FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
Cc FT TRANSMEM 178 198 POTENTIAL.
Cc FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
Cc FT TRANSMEM 247 267 CYTOPLASMIC (POTENTIAL).
Cc FT DOMAIN 268 336 N-LINKED (GLYCOPOLYMER) (POTENTIAL).
Cc FT CARBOHYD 95 95 T->A: NO EFFECT ON CHANNEL ACTIVITY.
Cc FT MUTAGEN 161 161
Cc SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;

RESULT 7
CIT1_MOUSE STANDARD; PRT; 336 AA.
AC 008581;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TWIK-1).
GN KCNK1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerogasthi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

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RX MEDLINE=97165959; PubMed-9013852;
RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
RA Lazdunski M.;
RT "The structure, function and distribution of the mouse TWIK-1 K+
RT channel.";
RL FEBS Lett. 402:28-32(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RX MEDLINE=98218573; PubMed=9559671;
RA Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;
RT "Structure, chromosome localization, and tissue distribution of the
RT mouse twik k+ channel gene.";
RL FEBS Lett. 425:310-316(1998).
CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
CC EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE
CC EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
CC CORTEX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
CC STABILIZES AFTER DAY 8.
CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC -----
DR EMBL: AF033017; AAC16973.1; -
DR MGD; MG1:109322; Kcnk1.
DR InterPro: IPR000099; -
DR InterPro: IPR001622; -
DR InterPro: IPR001779; -
DR InterPro: IPR003280; -
DR Pfam: PF02034; TWIK_channel.1.
DR PRINTS: PRO1096; TWIK1CHANNEL.
DR PRINTS: PRO1333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
FT TRANSMEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
FT TRANSMEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CAROHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 336 AA; 38275 MW; A996060A18266FD4 CRC64;

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Query Match 17.6%; Score 370.5; DB 1; Length 336;
Best Local Similarity 33.9%; Pred. No. 4.9e-18;
Matches 83; Conservative 57; Mismatches 94; Indels 11; Gaps 7;

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OY 51 FLVW--VYLIIIGATVFKLEQPHETISORTIVYKOTFISQSCNVSDELDELIOIYA 108
DB 25 FLVGLLTLVTEGAVVSEELPEYEDLLKQELKIKRRLFEHECLISEPOLDFLGRLVE 84

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OY 109 AINAGIIPLGNTSNOISHMDLGSPEFFACTVITIGFN 66EGGKIFCIYALLGIP 168
DB 85 ASNYGSVLSNMSGN-WMNDFTSALEFASVTLSTGYC 30LSDGKAPCIITISYIGIP 143
OY 169 LFGELLAGVGDOLGTIEGKIARKEDEFTIKMVSQTKI 111-FLLFGCVLFPALP 226
DB 144 FLLFLFTALVORTVAVTR--RPVLFHIRMGFSKOVMA 14VLLGFTVSCFFPI--P 199
OY 227 AIIFFKIE-GMSALDIYVVTITITIGRDYVAG-GS 14DPFKPVWMIYGLAY 284
DB 200 AAVFSYLEDMDNMFESFYCFSLSTIGLADYVPGGYV 14RELKIGITCYLLGLIT 259
OY 285 PAAVL 289
DB 260 MLVVL 264

RESULT 8
C1W3_HUMAN STANDARD; PRT; 394 AA.
AC 014649:
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACIF. POSITIVE POTASSIUM
DE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENS. IVE K+ CHANNEL).
GN KCNK3 OR TASK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97459932; PubMed-9312005;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations
RT near physiological pH.";
RL EMBO J. 16:5464-5471(1997).
RN [2]
RP ACTIVATION
RX MEDLINE=99254548; PubMed-10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Rom. G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE. BACKGROUND POTASSIUM
CC CHANNEL PROTEIN. RECTIFICATION DIRECTION IS NOT KNOWN. ACTS AS AN
CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST
CC EXPRESSION IN PANCREAS AND PLACENTA. LOW EXPRESSION IN BRAIN,
CC LUNG, PROSTATE, HEART, KIDNEY, UTERUS, AND COLON.
CC -1- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY
CC HALOTHANE AND ISOFURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF006823; AAC1777.1; -
DR MIM: 603220; -
DR InterPro: IPR000099; -
DR InterPro: IPR001622; -
DR InterPro: IPR003092; -

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DB 253 L 253

RESULT 10
C1W3_MOUSE STANDARD; PRT; 409 AA.

ID C1W3_MOUSE 035111; 035163;
AC 035111; 035163;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL)
GN KCNK3 OR TASK OR CTBAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98165556; PubMed=9506712;
RA Kim D., Fujita A., Horio Y., Kurachi Y.;
RT "Cloning and functional expression of a novel cardiac two-pore background K+ channel (CTBAK-1)."
RT Circ. Res. 82:513-518(1998).
RN [2]
RP SEQUENCE OF 4-409 FROM N.A.
RX MEDLINE=97459932; PubMed=9312005;
RA Duprat F., Lesage F., Fink M., Reyes R., Hurlbut C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations near physiological pH."
RT EMBO J. 16:5464-5471(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20287574; PubMed=10748056;
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT "Proton block and voltage gating are potassium-dependent in the cardiac leak channel kcnk3."
RT J. Biol. Chem. 275:16969-16978(2000).
RN [4]
RP FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
CC -----
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CC -----
CC EMBL; AB008537; BA25436.1; -
CC EMBL; AF006824; AAC3367.1; -
CC EMBL; AB013345; BAA2834.1; -
CC EMBL; AF241798; AAF81418.1; -
CC EMBL; AF242508; AAF81418.1; JOINED.
CC MGD; MGI:1100509; Kcnk3.
CC InterPro; IPR000099; -
CC InterPro; IPR01622; -
CC InterPro; IPR003092; -

DR InterPro; IPR003280; -
DR Pfam; PF02034; TWIK_channel; 1.
DR PRINTS; PRO1095; TASKCHANNEL.
DR PRINTS; PRO1333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 9 29 POTENTIAL.
FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).
FT TRANSMEM 108 128 POTENTIAL.
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 POTENTIAL.
FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).
FT TRANSMEM 223 243 POTENTIAL.
FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 4 4 O -> E (IN REF. 2).
FT CONFLICT 123 123 V -> I (IN REF. 2).
SQ SEQUENCE 409 AA; 45068 MW; 35236E01AACE 87 CRC64;

Query Match 16.3% Score 343; DB 1; Length 409;
Best Local Similarity 29.9%; Pred. No. 4, 1e-15;
Matches 88; Conservative 62; Mismatches 102; Indels 42; Gaps 9;

QY 42 MKKRVSTFLVY--VLVLIIGATVFKALQPHETISQRTIVIQKOTFSQSCVNS--T 97
DB 1 MKRQNVRTLLALVCFPTVLLVGAAVFDALSEPEMERORILRLQELARVNLSCGYE 60
QY 98 ELDELIIQIVAAIMAGIIFLGNSTNOISHWDLGSSFFPAGVYTTIGFQGNISPREGGKI 157
DB 61 ELERVVLR--KPKKAGV-----QMRPAGSYFYFAITVITTYIGHAAPSTGSKY 108
QY 158 FCIYVALLGPILEGFLAGVGDLGTFPKGIAKVEDFT--NVSTK-----IRI 208
DB 109 FCFYVALLGPIPLTVLFGSLGERT-----NT--LILHAKKGLGNRAEVSVM 156
QY 209 ISTIIFILGCVLFAVLPATIFKHIEGMSALDAIYFVV--L--TIGRGDVAGGSD--IEY 266
DB 157 ANNVILGFSCSTLCIGAAFSYERMTFFPAPYICF--L--TIGGDVVALQKQALOT 216
QY 267 LDFYKPVVFWILVGLAYPAVLSMIGDLRVYISKRTKTVVEEFRAHAWEWTAN 320
DB 217 QPQYAFSEVYVILGLTVIGAFNLNV--VLRMTMAEDEKRD--AEHRALLTHN 257

DB 217 QPQYAFSEVYVILGLTVIGAFNLNV--VLRMTMAEDEKRD--AEHRALLTHN 257

RESULT 11
C1W3_MOUSE STANDARD; PRT; 411 AA.

ID C1W3_MOUSE 054912;
AC 054912;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
GN KCNK3 OR TASK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=98099797; PubMed=9437008;
RA Leonoudakis D., Gray A.T., Winegar B.D., Kinsler C.H., Harada M., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum."
RT J. Neurosci. 18:868-877(1998).
RN [2]
RP FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.";
 CC Nature 368:32-38(1994).
 CC -i- SIMILARITY: TO POTASSIUM CHANNEL PROTEIN HAK-6.
 CC -----
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 CC -----
 CC EMBL: L12018; AAA65460.1; -
 CC WormBEP: F22B7.7; CE00160.
 CC DR
 CC SO SEQUENCE 335 AA; 38472 MW; 27DE7F1E79B3CA29 CRC64;

Query Match 10.4%; Score 217.5; DB 1; Length 335;
 Best Local Similarity 26.7%; Pred. No. 7.7e-08;
 Matches 60; Conservative 37; Mismatches 75; Indels 53; Gaps 7;
 OY 120 TSNQISH-----WDLGSSFFRAGVYTTTIGFNGNISPRTEGKIFCIYALLGIPLEGFL 173
 DB 15 TSNEVKKRNATETWTFSSSIFFAVVTVTIGYGNPVPVNTNIGRIMCILFSLGIPL---T 71
 OY 174 LAGVGDLGTIRGKIFAKVEDPFIK-----NNVSQT 204
 DB 72 LVTIAD-LKFLSEHLVWLXGNTLKLKYLILSRHKKRERHVCCHSHGMGHDNMIIEK 130
 OY 205 KIRIISFIIFLFGCVLFAVLPALIPKHIKIGWSALDAIFYVVTITTTIGFGDYVAGGSDI 264
 DB 131 RI----PAFLVLAIIIVYTAFGVLSKLEPMSEFTSFYWSFITMTYVGGDLMPRRDGY 186
 OY 265 EYIDF-----YKPVVWFILVGLAFPAVLSMIG--DWLRVI 299
 DB 187 MYILLYIILGKFSMKKOKFKIFIGLAIYTMCIDLVGVQYIRKI 231

Search completed: August 28, 2001, 17:13:13
 Job time: 407 sec